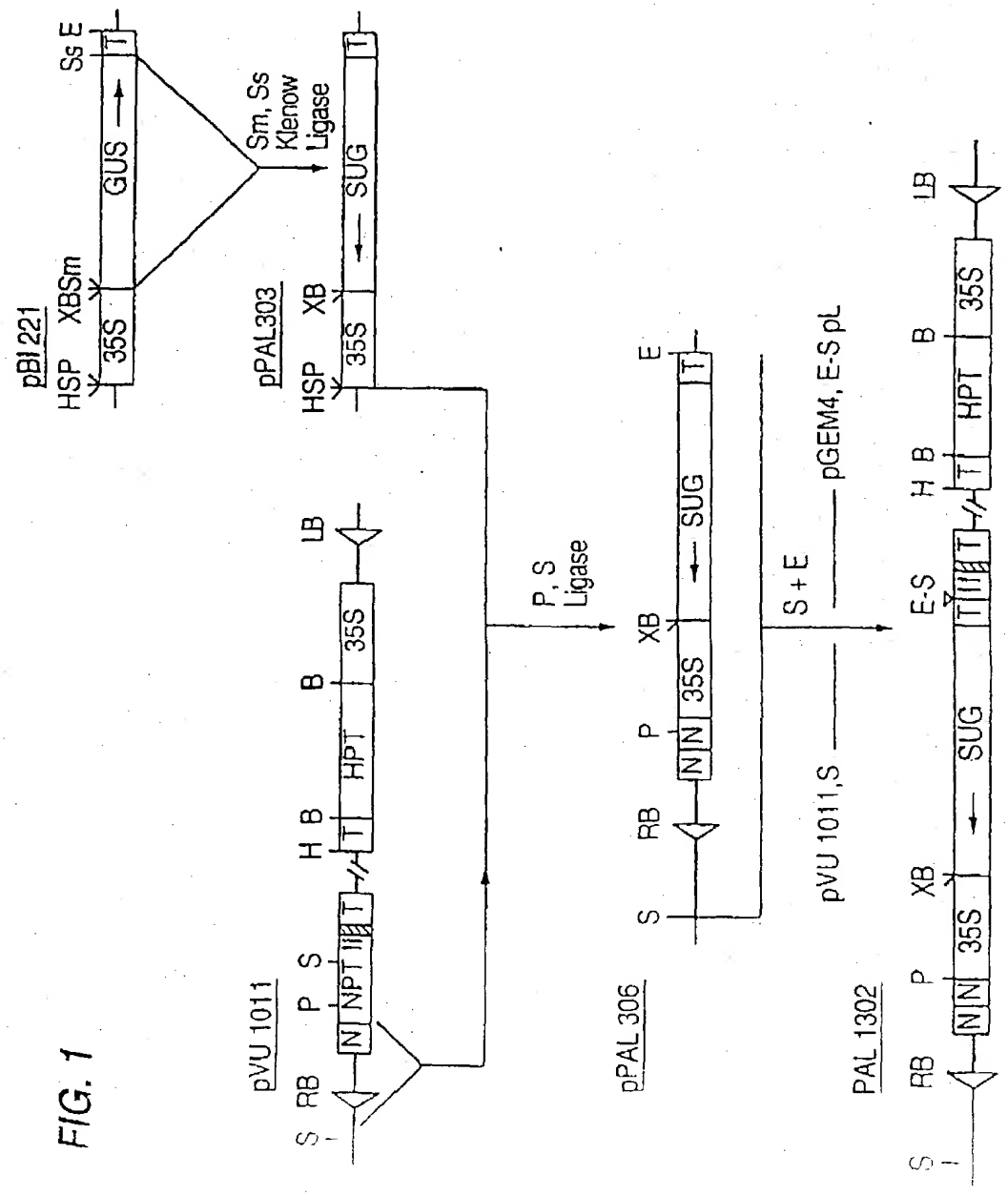
08/484838

FIG. 1



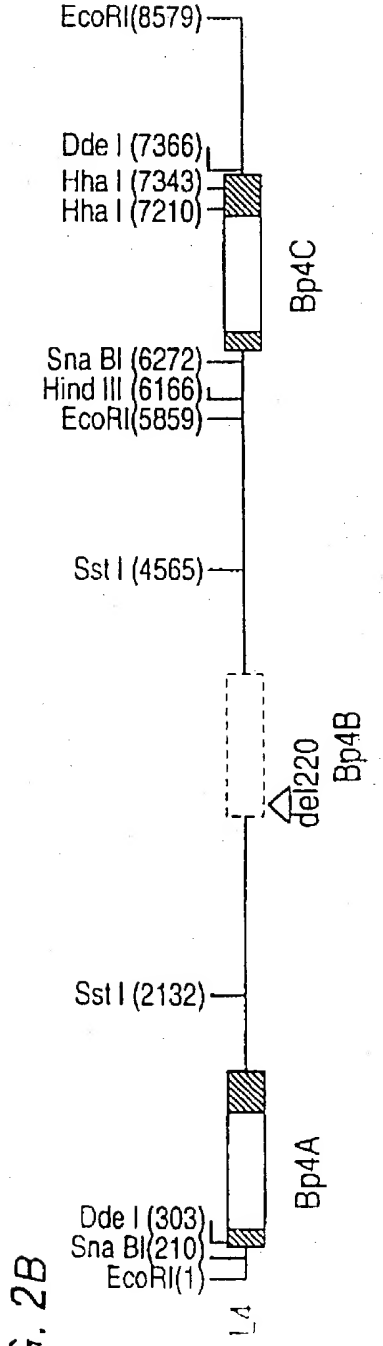

EcoRI(8579)
Dde I (7366)
Hha I (7343)
Hha I (7210)
Bp4C
Sna BI (6272)
Hind III (6166)
EcoRI(5859)
Sst I (4565)
del220
Bp4B
Sst I (2132)
Bp4A
Dde I (303)
Sna BI(210)
EcoRI(1)

FIG. 2B

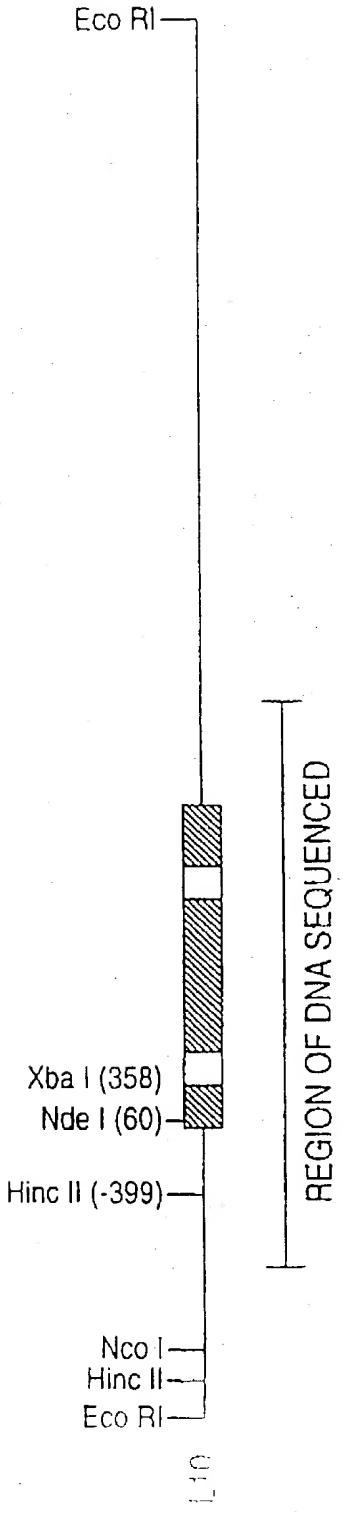

Eco RI
Xba I (358)
Nde I (60)
Hinc II (-399)
Nco I
Hinc II
Eco RI
REGION OF DNA SEQUENCED

FIG. 2A

FIG. 2D

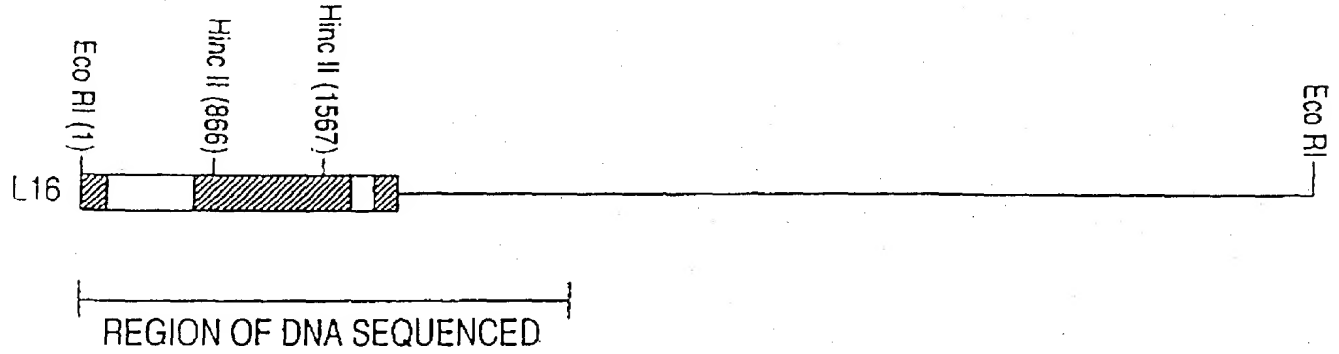

Eco RI (1)
Hinc II (866)
Hinc II (1567)
Eco RI
L16
REGION OF DNA SEQUENCED

FIG. 2C

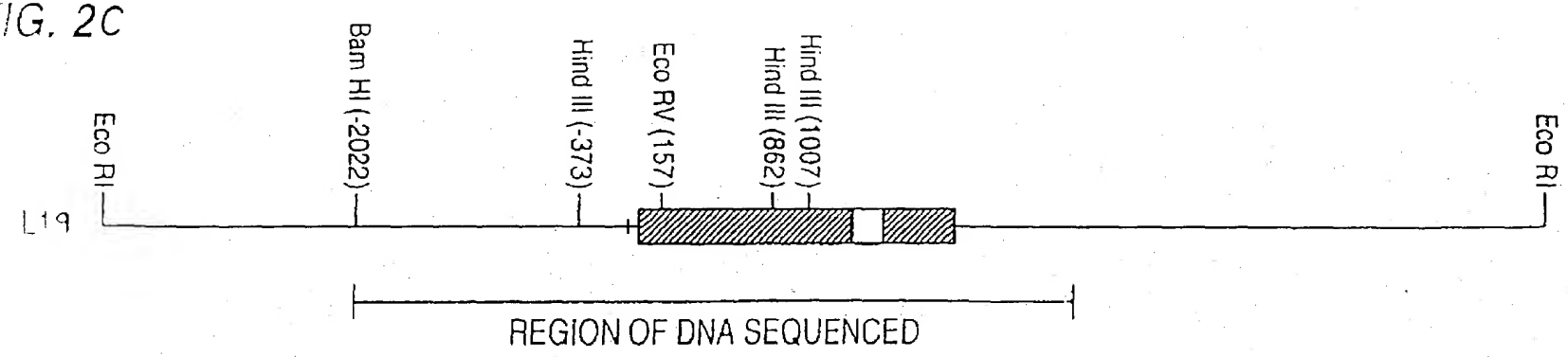

Eco RI
Bam HI (-2022)
Hind III (-373)
Eco RV (157)
Hind III (862)
Hind III (1007)
Eco RI
L19
REGION OF DNA SEQUENCED

FIG. 3A(1)

```
1    GAATTCTAAAAATAGCAATAACTTTTTGAGAACATCAGATTTATGTACACGCATAGGACA    60

61   CATACCTTTTTATTTACTTAAAGGAAAATGAACGAGTCTAAATCTTCCACATGTTATATG    120

121  AGCAAAACATGAATTTTTCTAAATTAGATTCGTTTAAATCAGAACATATTAATGTGAGTT    180

181  TCTTAAATTAGATTTTTAATATCTATATATACGTAAGAATACTTCTTATGTTTTAAAATA    240

241  AAAAATAGAATACTTCATCTCTTTCCTAAATTTTTAAGCCAATATCAATCCATTTCTATA    300

301  ATCTAAGATGAAGAAATCCCTTCAACTCTCTTTTTCGTTCTTAATTATCTCCATCATTCT    360
           M  K  K  S  L  Q  L  S  F  S  F  L  I  I  S  I  I  L

361  CTCACATGGTTTGTATTTTCATCTTAATATATTGCATATAGTAATTCCATAATAAATTGA    420
       S  H  G

421  TTATACTAAAATTTGACTTTTAAAATATTGTCAACCCCCATATAATAAATTTTATTTACT    480

481  ATATAAAACATAGCATTAAATTATCTCTTTGTGTAAAATTCATAACTTTGCAGAAGGCTA    540

541  GAAAATATAGATAGTATAGTCAGAAATGTTTGCGTTAAAATTGAAAGGATCAACCATGGA    600

601  GTATTTAAATGTTTTTTATACTTTATGCCATTTATAATTTTTTTAATGTATGGGTTTATA    660

661  TATGATGAAGAACTATTATGATAAAATAATATTAAATAATTTCATTTTTATCATCTATTT    720
```

FIG. 3A(2)

```
721  ATGAACATTTTGTCCTGCACATACAAATGATTTAACCAACATTTTTAATAATATGGATGA  780

781  ACTATAGCTCTTACGTAAATTTATTGATATTTTTAATTAAATTTATATATTTTTATAGG  840

841  TAATTTGTTATGCTTTTCCAATACATACAGTAGTTGTTATTAAAATATCAAAATTTAATA  900

901  CGTAATGTTTATTAATATGCACACAATTCTTAAAACCATATTTTTAAAAAATAATGTGTG  960

961  ACCAAACGATATGCTCATTTTTTTATTTACTAGCAAAATATATTTCTTTTCTTACTTATA  1020

1021 ACGTTTAAAAAGAAATGTTATTAAACATTTTTTGCTGATAAATAAATTTTATATTTCATA  1080

1081 AAATCTAAATATATTTTTTAACAATTAAAATTTGAAATTTTTATATCTTACAGGAATGAT  1140
                                                        M  M

1141 GGCAGATGCGCAGAAAAAGAATTGTCCTCATAAAATTCCAATAAAAGGAAGTTATTGTGC  1200
       A  D  A  Q  K  K  N  C  P  H  K  I  P  I  K  G  S  Y  C  A

1201 TCCAACTATATGTTTGGATATGTGTAAGAAGCAACATGGAACTGTTGGTAGTTGTGCGGA  1260
       P  T  I  C  L  D  M  C  K  K  Q  H  G  T  V  G  S  C  A  E

1261 ATAAAAATGATTTTGTAACTGCGCTTGTAAGTAAGGGTTCTCACTAAGTGTTATGAATCT  1320
       STOP
```

FIG. 3A(3)

1321	AGTAATGTCCAACCAAAGTTTTATATTATTTCTTTTAACAATAAGTCTAAATGTTTGTCT	1380
1381	CAGATTTGTGGATCTATTTATAATAAATAATAATATGAATGTTAAATAAATACAAATGTG	1440
1441	TAAAACAAGAGTGGACTATTAATAAAATATATGATTACATTATTGTTAGAAGTAACCAAT	1500
1501	ATTACGTGTAAAATCAAAATCTTAAGACAAGTTAAAAAAGATTGAGATGAAATCACAACCA	1560
1561	ATATTTAAATGTGAGATAATCAACTAACATGTAATTTTGTACACATTGTAAAAAAAAAAA	1620
1621	AGCAAGAGTTCATTATCAAACAAGAAAGTGTTAGAAAGAGCAACAGATTCATTGCAAGGG	1680
1681	CAGTCTAGGTTGAATTGGCTTGACATAGGGAAAATTGAAAGCACTGTTTCTGAACATGAC	1740
1741	AACGCTTGGTCAGGAAGAACAATCTCACAACCAGAGTTTTGGGTAGATTTCTCCAATGTC	1800
1801	ATTATCAGGTACGAGTTATGAGACTTCATCCACATCTCAGTCCCAGTTCCCTTCTCAGGA	1860
1861	AGTTTCCTTGAGGAAGGAGGTTATTACAGAAAGCTAAGTTACATGAGCCTGACATATCAT	1920
1921	GCAAGGGCAGTCCCAACAAGAAAATGTTAGAAAGAGCAACATATCATGCAAGGACAGTCC	1980
1981	AGGTTTGAATTGGCTTGACAGATGGTTTGCAGACATGCCATCTGAAGGTCCTACAAACTC	2040
2041	ATCAGACAACGAAGGAAAATTGATAGCATTGTTTCTGAACATGACAAAACTCTAGTCAGG	2100

FIG. 3A(4)


2101 AAGAAGAATCTCACAACCAAAGTTTTGGGTAGAGCTCCTCCAATGTCATCATCAGCTACG 2160
2161 AGTTCAAAGACTTCATCCACATCTTAGTCCCCATTCTCTTCTCATGAAGTTTCCTTTAGG 2220
2221 AAAGAGGTTATTACAGAAAGCCAAGTTACATGAGCCTAACACAATCTATCAAAGCTAAGA 2280
2281 AGAGACGATTAACCATTATTCTTCATCTTTTTGTCCCAAAATCACTGTTTGAAAAGAAAC 2340
2341 AGTCCATGTCTTACAACGAAGATGTGAATGTAAAGCGTTGTGCATGTTCGGATCCATCTT 2400
2401 GCAACCAGCAGAGTTATCTATATCCACATGCTCAAGTAACAAGGAAAAATATGTGGCCAA 2460
2461 AGAAGGTAAAGTGAACATCGTTTCATTAATTCATTAAAGCATTTCAACACCTTGATGGTT 2520
2521 CTAAATACACACAAAACACTGATTTATAGATACATAAGCAACTTCTGTGTATGTTCTTTT 2580
2581 ACATACAAGTTGGTATCAAGGCTGTTGCAATGTTGTTGTTTGACCACTTTTATTATTTAA 2640
2641 TAGTTAACTTTTGATGCTTCTAAGATAATATGTTCCTCCTAACTCTTGTCAACATGAAAG 2700
2701 ACCAATTAAAGGTTTTGATTAAATACATACTAATTTTTTAATATAATCTTATAAGTTATG 2760
2761 TTACGTGTGGGACATCCACCTAATAAACTATAAATTTAAATAATAATGTTTGAAAAGGAT 2820

FIG. 3A(5)


2821 TTTATTGACATTCCTTTAAATAAATTCATAATTTTAAAAATAGCGATAACTTTTTGAAAA 2880
2881 CATCAGAATTATGTACACGCAGAGGACACATACCTTTTTTATTTACTTATAGGAAAATGAA 2940
2941 CGAGTCTAAAGCTTCCACATGTTATATGAGCAAAACATGGATTTTTCTAAATTAGATTCG 3000
3001 TTTAAATCAGAACATATTAATGTAAGTTTCTTAAATTAGATTTTTAATATGTATATATAT 3060
3061 GTAAAAATACTTCTTTTTTTTTTTTTTGTCATCAGCATTACAGATTTCTAAATAAGTTAC 3120
3121 TTCTTATGTTTTAACAAATAGAATACTTCATCTCTTTCCTAAATTTTAAGTCAATATCAA 3180
3181 TCCATTTCTATAATCCGAAGATGAAGAAATCCCTTCATCTCTAGAAAATAGGGTCAGAAA 3240
3241 GTTTTGCGTTAAAATTGAAAGGATCATCCCTGAAGTATTTATTTGTTTTTTTTATGCTTT 3300
3301 AGTCCATTAATATTTTTTTAATGTATGGGTTTATATATGATTAAGAACTTCCATGATAAA 3360
3361 ATAATATTAAATAGTTTTATTTCTTATCATCTATTTATGAACGTTTGTTCCTGCACACAC 3420
3421 AAATGATTTAACCAACATTTTTCATAATATGGATAAACTATAGTTCTTATGTAAATTTAT 3480
3481 GTGATATTTTAATTAGATTTATATATTTATAGGTAATCTATTATGCTTTTCCAATACATA 3540
3541 CAGTAGTTGTTCTTAAAACATCAAATTTTTATATGTAATGTTTATTAATATGCACACAAT 3600

FIG. 3A(6)

3601	TCTTAAAACAATATTTTCACAACATAAAAAAATAATGTTTGACCAAACCATATGCTCATT	3660
3661	TTCTTTATTTACCGGCAAAAACCATTTCTCCATTTTTTTACTTATAACGCTTAAGATAAA	3720
3721	AAAATTATTAAACAGTTTTTGTTGATAAATAAGTTTTATATTTCAGAAAATGTATTATAT	3780
3781	TTTCAAACAATTAAAATTTGGGTTTTTATATCTAACATAAATGATGGCAGAAGCACAGAA	3840
3841	AAATAATTGTCTTCATAAAATTCCAATAAAAGGAAGCTAGTGCATTCCAAATAAATGTTT	3900
3901	GGCTATGTGTAAGAAGCAACATGGAACTCTTGGTAGTTGTCCGGAAAAAGAAATTTGTAG	3960
3961	TTGTGCTTGTAAGTAAGGGTTCTCACTAAGTGTTATGAATCTAATAATGTCCAACCAAAG	4020
4021	TTGTATATAATTTTTTAACAATAAATGTCTAAATGTTTGTCTCAGATTTGTGGATCTATT	4080
4081	TATAATAAATAATAATATGAATGTTAAATAAATACAAATGTGTAAAAAAAGATTGGACTA	4140
4141	TTAATAAAATAAATGATCACATTATTATTAGATGTAACCAATATTGTGTATAAGATCGTA	4200
4201	AAAGCTTAAGACGAGTTAAAAAGATAGAGATGAAATCACATCCAATATCTAAATGTGAGA	4260
4261	TAATCAACTAACATATAATTTTGTATATATTGTAAGATAAAATAAAAATAAAAATTAAAA	4320

FIG. 3A(7)

```
4321  AGCAAGAGTTGATTATCAAACAAAGAAGTATTAGAAAGAGCAACAGATCATGCAAGAAGA  4380
4381  GTCCATGTTTGAATTTTCTTGACAGATGGGTTGCAGACAAGTCATGGGAAGGTCATACAA  4440
4441  ACTCATCAGACAACGCAAAGAAAATTGATAGCACAGTTTCTGAACATGACAAAGCTCTGG  4500
4501  TCATGAAGAACAATCTCACAAGCAGAGTTTTGGGTAGACCTCCTCCAATGTCATCATCAG  4560
4561  CTACGAGCTCTGAGACTTCATCCACATCTCAGTCCTCAGTTTCTTCCCAGGAAGTTTCCT  4620
4621  TGAGGAAGGAGGTTATTACAGAAATCCAAGTTACATGAGCCTGGCAAAATCTATCAAAGC  4680
4681  TAAGCAGAGATGATCACGGTATTCTTCATCGTCTTCTTCCAAAACCTGGTTTGAGAAAAA  4740
4741  ACAATCCATGTCTTACAACAGAGATGTAAATGTAAAGTGTTGTGTTTGTTCGGATCAATC  4800
4801  TTGCAACCAGTGGAGTGATCTATATCGACCGGTTCAAGTAACAAGGAGAACTATGTGGGA  4860
4861  AAGAGGCTAAATTAAACATCGTTTCATCAAAGATTGTTGCAATGTTGTTGTTTGGCCACT  4920
4921  TTGATTATTTAATAATTAACTTCGGATGCTTCTGAGACAATCTGTTCCTCCCATTTTTTG  4980
4981  TCAATATGAAACGAAGAGCAATGCTTCATCTTTAGACATGAAAAGCCATTTAAATGACCA  5040
5041  AATAACATAGTTTATACCAAAGCTTCCTTATAAATTTTACCCGTTCTAAAAATTGCTCTT  5100
```

FIG. 3A(8)


5101 ACTATCAAAATCTAAAACTGAATTAAATTCAATTATCTTACTGTTACACAGTTTTCACTA 5160
5161 ATCACTATTTTAATGTATAAACTATAAAAATAAATTAAATACTTACTAAATTTTTAGATT 5220
5221 TAATCCATAAATTATATTACAGTTCAGAGATTTCATCCACATTTCAGTCCCCAGTCCCTT 5280
5281 ACTCATTAAATTTTCCTGAGGAAGGAGGTTATACAGAAAGTCAACTTACATGAGCCTTAC 5340
5341 TCAATCTATCAAAGCTAAGAAGAGATGTCAGGTTCTTCTTCATCTTTCTGTTCCACATCA 5400
5401 CCATTTAAGTAGAAACAGTATATGTCTTACAACGGTGATGTGAATGTAAAGGGTTGTGCT 5460
5461 GGTTCGGAGTAGACTGATCTATATCCACCAGTGCAAGGAACATGGAGGCATATGTGGGCT 5520
5521 AAAAAAAACATCATTAACTGAATCTTTAAAGCACTTTCAACATCTTGTTGGTTCCATGAA 5580
5581 ATACATAAATGGATTATAGGTTATTGAAGCCATTGTTGTATATGTTTCTTACTTATAAAT 5640
5641 TAGTTTGAAGACAGCAATGTTGTTGTTTGGCCACTTTGATTATTTAATAATTAACTTCTG 5700
5701 ATCTTTCTGAGACAATATGTTCCTCTTATTTCTTGTCAATATGAAACCAAGAGCAAAGTT 5760
5761 TCATCCTTAGACATGAAAGGCTTATTAAATGACCAAATAACATAGTTTAGACGAAAGCTT 5820

FIG. 3A(9)

```
5821  CCTAATAAAATTTATTCTCACTATCTAAATCTAAAACTGAATTCAATTCATCTATCTGAT  5880
5881  TATTATATAGTTTTCATTTTTTGTTATTTTATTGAATGAGTAAAAAATTTAATTAAATAC  5940
5941  TTACTATTTTTTTTCATATAATCTTATAAATTATGTTACGTGTGGGACATCCACCTAATAA  6000
6001  CCTATTAATTTAAATAGTAATATTTGAAAAATATTTTATTGACATTGTTTTAAATAAATT  6060
6061  CATAATTCTAAAAATAGCAATAACTTTTTGAAAACATCAGATTTATGTACACGCATAGGA  6120
6121  CACATACCTTTTTATTTACTTAAAGGAAAATGAACGAGTCTAAAGCTTCCACATGTTATC  6180
6181  TGAGCAAAACATGGATTTTTCTAAATTAGATTCGTTTAAATCAGAACATATTAATGTGAG  6240
6241  TTTCTTAAATTAGATTTTTAATATGTATATATATACGTAAGAATACTTCTTATGTTTAAAAA  6300
6301  AAAAAATAGAATACTTTATCTCTTTCCTAAATTTTTTAAGCCAATATCAATCCATTTCTAT  6360
6361  AATCCAAGATGAAGAAATCCCTTCAACTCTCGTTTACGTTCTTAATTATCTCCATCATTC  6420
                M  K  K  S  L  Q  L  S  F  T  F  L  I  I  S  I  I  L
6421  TCTCACAAGGTTTGTATTTACATCTTAATATATTGCATATAGTAATTCCATAATAAATTG  6480
        S  Q
6481  ATTATACTAAACTTTGACTTTTAAAATATTGTAAACCCCCCATATAATAAATTTTATTTA  6540
```

FIG. 3A(10)

```
6541  CTATATAAAACATAGCATTAAATTATCTCTTTGTGTAAAATTCATAACTTTGCAGAAGGG  6600
6601  AAGAAAATATAGAAAGTATGGTCAGAAATGTTTGCGTTAATATTGAAAGAATCAACCCTG  6660
6661  AAGTATTTAACTGTTTTTTATACTTTATGCCATTTATAATTTTTTTAATGTATGGGTTTA  6720
6721  TATATGATGAAGAGCTATTATGATAAAATAATATTAAATAGTTTCATTTTTATCATCTAT  6780
6781  TTACGAACATTTTGTCTTGCACATACAAATGATTTAACCGACATTTTTCATAATATGGAT  6840
6841  GAACTATAGTTCTTACGTAAATTTATTTGATATTTTTAACTAATTTTATATATTTTTATG  6900
6901  CTTTTCCAATACATACAGTAGTTGTTCTTAAAATATCAAAATTTTATACGTAATGTTTAT  6960
6961  TAATATGCACACAATTCTTAAAACCATATTTTTCACAAAATAAAAAATAAAGTGTGACCA  7020
7021  AACGATATGCTCATTTTTTTTTATATACTGGCAAAATATATTTCTTTTTTTTTTTACTTA  7080
7081  TAACGTTTAAAATGAAATGTTATTAAACATTTTTTGCTGATAAATAAATTTTCTATTTCA  7140
7141  TAAAATCTATATATATTTTCTAACAATTAAAATTTGAAATTTTAATATCTTACAGGAATG  7200
                                                                  M
7201  ATGGCAGATGCGCAGAAAAAGAATTGTCCTCGTAAAATTCCAATAAAAGGAAGCTATTGT  7260
```

FIG. 3A(II)

M A D A Q K K N C P R K I P I K G S Y C

7261 GCTCCAACTATATGTTTGGATAAGTGTAAGAAGCAACATGGAACTGTTGGTAGTTGTGCG 7320

A P T I C L D K C K K Q H G T V G S C A

7321 GAAGAAAAAGGATTTTGTAACTGCGCTTGTAAGTAAGAGTTCTCACTAAGTGTAATGAAT 7380

E E K G F C N C A C K STOP

7381 CTAGTAATGTCCAACCAAAGTTTTATATTATTTCTTTTAACAATAAGTCTAAATGTTTGT 7440

7441 CTCAGATTTGTGGATCTATTTATAATAAATATTAATATGAATGTTAAATAAATACAATTG 7500

7501 TATAAAACAAGAGTGGACTATTAATAAAATATATGATCACAGTATTGTTAGAAGTAACCA 7560

7561 ATATTACGTGTAAAATCAAAAGCTTAAGACTAGTTAAAAATATAGAGATGAAATCACAAC 7620

7621 CAATATTTAAATGTTATATAATCAACTAACATGTAATTTTGTACACATTGTAAAAAAAAA 7680

7681 AAAAAAAAAAAAAAGCAAGAGTTGATTAACAAACAAGAAAGTGTTAGAAAGAGCAACAGA 7740

7741 TCATGCAAGAGCAGTCTAGGTTTGAATTGGCTTGACAGATGTGTTGCAGACATGCCATGA 7800

7801 GGAAGTCTTACAAACTCATCAGACAACACACAGAAAATTGATAGCATTGTTTCTGAACAT 7860

7861 GACAAAGCTCTGGTCATGAAGAAAAATTTCACAGCCAAAGTTTTTGGTAGACCTTCTCCA 7920

FIG. 3A(12)

7921 GCTACGAGTTTTGAGACTTCATCCACATCTCAGTCTCCATTTCCATTCTCATGAAGTTTT 7980

7981 CTTTAGGGAAGAGGTTATTACAGAAAGCCAAGTTACATGAACCTAACACAATCTATCAAA 8040

8041 GGTAAGAAGAGACGATCAACCAGTATTCTTCATCTTCTTGTTCCGAAATCACTGTTTGAA 8100

8101 AAGAAACAGTCAATGTCTTACAACGAAGATGTGAATGTAAAGTGTTGTGCATGTTCGGAT 8160

8161 CCATCTTGCACCCAGTGGAATGATCTATATCTACATGCTCAAGTAACAAGGAGAAATATG 8220

8221 TGGGCAAAGAAGCTAAAGTAAACATTGTTTCATTAAATCTTTAAAGCATTTCAACACCTT 8280

8281 GAGAGTTCTAAAACACACACAAAATACCGATTTATAGATATATAAGCAACTTCTATGTAT 8340

8341 GTTCTTTTACATACGAGTTAGTATGAAGACTGCTGCAATGTTGTTGTTTGACCATTTTTA 8400

8401 TTATTTAATAGTTAACTTCTGATGCTTCTAAAATAATATGTTCTTCCCAACTCTTGTCAA 8460

8461 TATGAAACCAAGAGCAAAGTTTTAATTTTAGACATGAAACGCCTATTAAATGACCAAATA 8520

8521 ACATAGTTTAGACGAAAACTTCCTAATAAAATTTATTCTCACTATCTAAATCTAAAACTG 8580

8581 AATTC 8585

FIG. 3B(1)

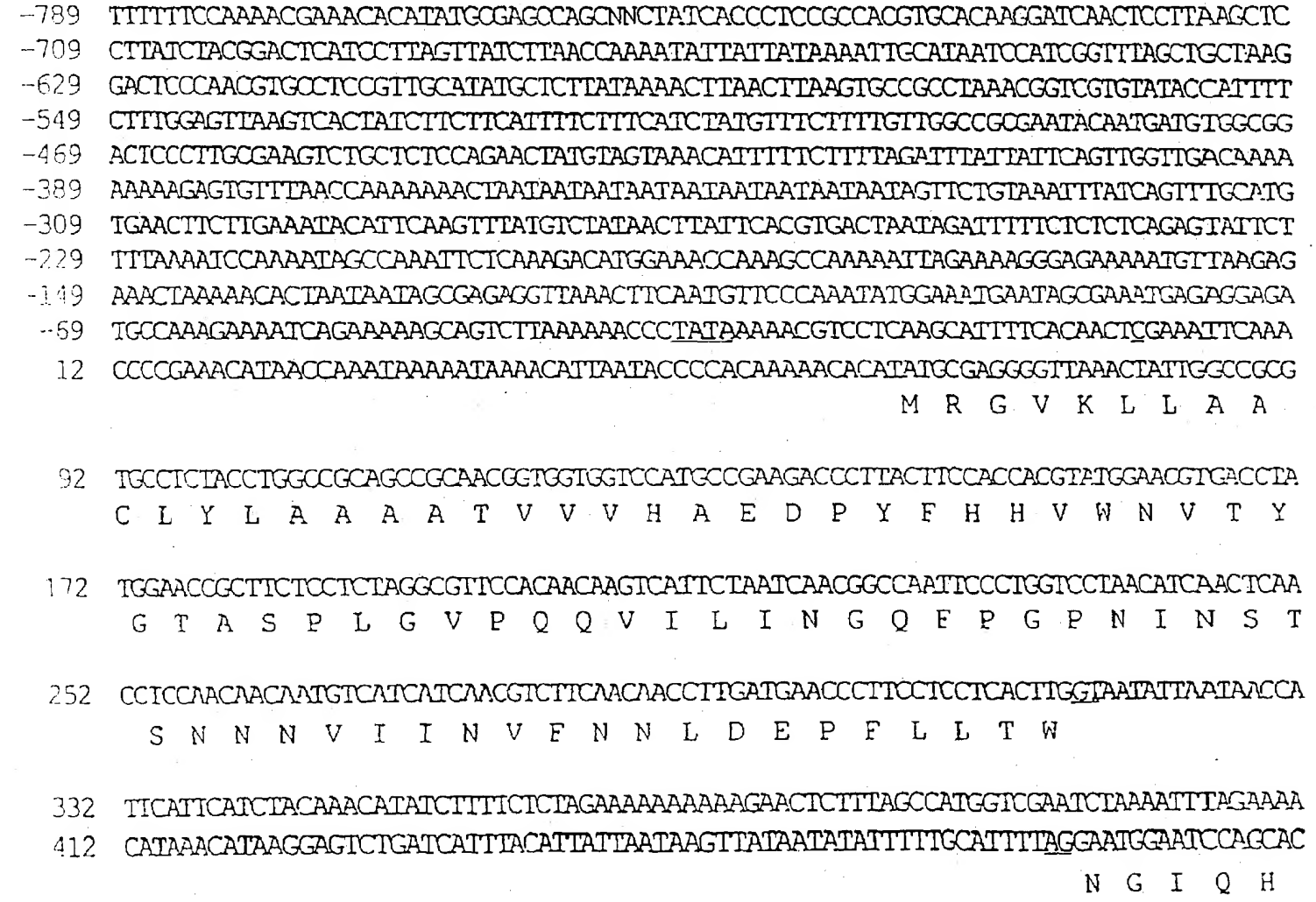

-789 TTTTTTCCAAAACGAAACACATATGCGAGCCAGCNNCTATCACCCTCCGCCACGTGCACAAGGATCAACTCCTTAAGCTC
-709 CTTATCTACGGACTCATCCTTAGTTATCTTAACCAAAATATTATTATAAAATTGCATAATCCATCGGTTTAGCTGCTAAG
-629 GACTCCCAACGTGCCTCCGTTGCATATGCTCTTATAAAACTTAACTTAAGTGCCGCCTAAACGGTCGTGTATACCATTTT
-549 CTTTGGAGTTAAGTCACTATCTTCTTCATTTTCTTTCATCTATGTTTCTTTTGTTGGCCGCGAATACAATGATGTGGCGG
-469 ACTCCCTTGCGAAGTCTGCTCTCCAGAACTATGTAGTAAACATTTTTCTTTTAGATTTATTATTCAGTTGGTTGACAAAA
-389 AAAAAGAGTGTTTAACCAAAAAAACTAATAATAATAATAATAATAATAATAATAGTTCTGTAAATTTATCAGTTTGCATG
-309 TGAACTTCTTGAAATACATTCAAGTTTATGTCTATAACTTATTCACGTGACTAATAGATTTTTCTCTCTCAGAGTATTCT
-229 TTTAAAATCCAAAATAGCCAAATTCTCAAAGACATGGAAACCAAAGCCAAAAATTAGAAAAGGGAGAAAAATGTTAAGAG
-149 AAACTAAAAACACTAATAATAGCGAGAGGTTAAACTTCAATGTTCCCAAATATGGAAATGAATAGCGAAATGAGAGGAGA
-69 TGCCAAAGAAAATCAGAAAAAGCAGTCTTAAAAAACCCTATAAAAACGTCCTCAAGCATTTTCACAACTCGAAATTCAAA
12 CCCCGAAACATAACCAAATAAAAATAAAACATTAATACCCCACAAAAACACATATGCGAGGGGTTAAACTATTGGCCGCG
M R G V K L L A A
92 TGCCTCTACCTGGCCGCAGCCGCAACGGTGGTGGTCCATGCCGAAGACCCTTACTTCCACCACGTATGGAACGTGACCTA
C L Y L A A A A T V V V H A E D P Y F H H V W N V T Y
172 TGGAACCGCTTCTCCTCTAGGCGTTCCACAACAAGTCATTCTAATCAACGGCCAATTCCCTGGTCCTAACATCAACTCAA
G T A S P L G V P Q Q V I L I N G Q F P G P N I N S T
252 CCTCCAACAACAATGTCATCATCAACGTCTTCAACAACCTTGATGAACCCTTCCTCCTCACTTGGTAATATTAATAACCA
S N N N V I I N V F N N L D E P F L L T W
332 TTCATTCATCTACAAACATATCTTTTCTCTAGAAAAAAAAAAGAACTCTTTAGCCATGGTCGAATCTAAAATTTAGAAAA
412 CATAAACATAAGGAGTCTGATCATTTACATTATTAATAAGTTATAATATATTTTTGCATTTTAGGAATGGAATCCAGCAC
N G I Q H

FIG. 3B(2)

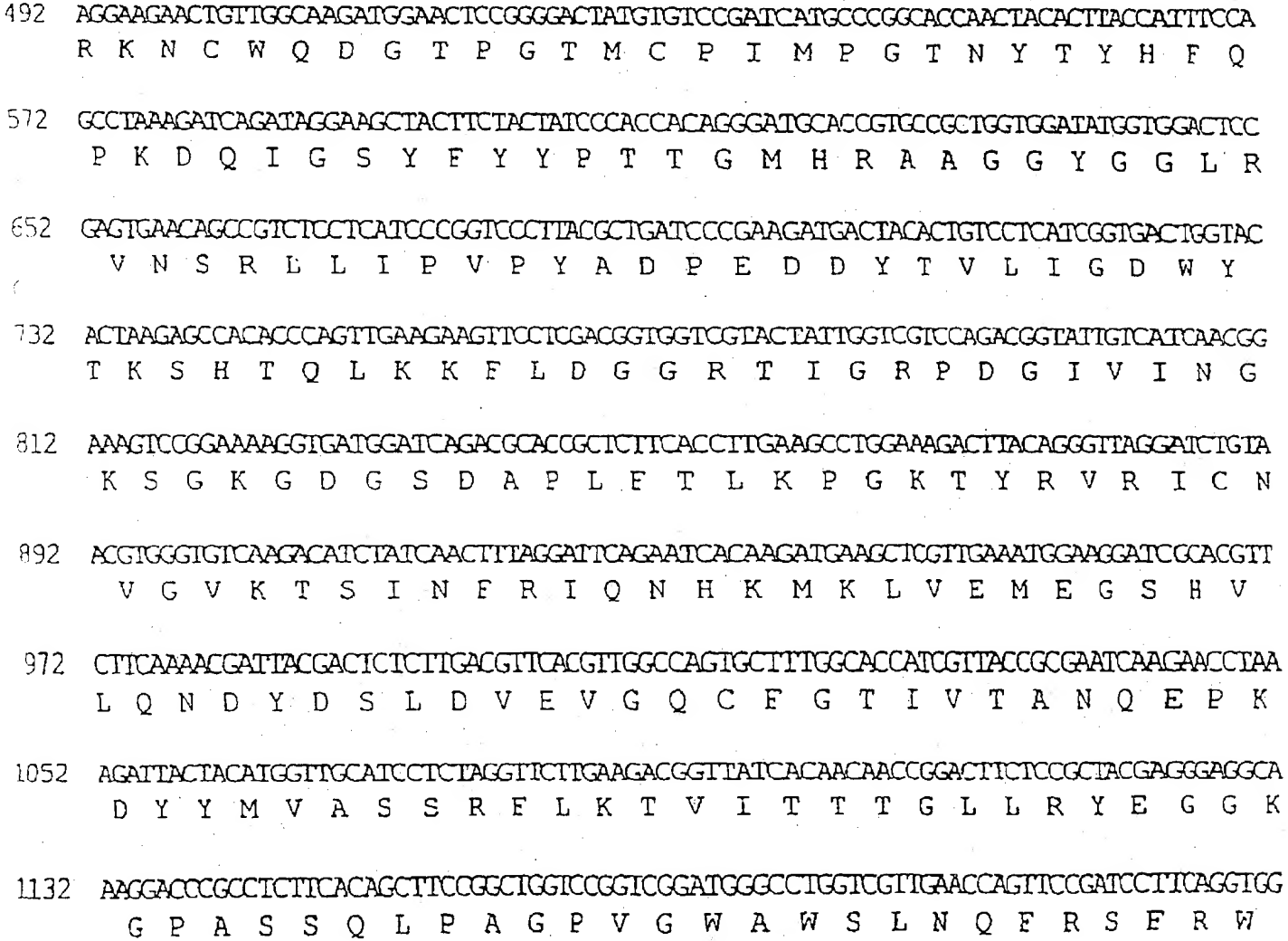

492 AGGAAGAACTGTTGGCAAGATGGAACTCCGGGGACTATGTGTCCGATCATGCCCGGCACCAACTACACTTACCATTTCCA
R K N C W Q D G T P G T M C P I M P G T N Y T Y H F Q
572 GCCTAAAGATCAGATAGGAAGCTACTTCTACTATCCCACCACAGGGATGCACCGTGCCGCTGGTGGATATGGTGGACTCC
P K D Q I G S Y F Y Y P T T G M H R A A G G Y G G L R
652 GAGTGAACAGCCGTCTCCTCATCCCGGTCCCTTACGCTGATCCCGAAGATGACTACACTGTCCTCATCGGTGACTGGTAC
V N S R L L I P V P Y A D P E D D Y T V L I G D W Y
732 ACTAAGAGCCACACCCAGTTGAAGAAGTTCCTCGACGGTGGTCGTACTATTGGTCGTCCAGACGGTATTGTCATCAACGG
T K S H T Q L K K F L D G G R T I G R P D G I V I N G
812 AAAGTCCGGAAAAGGTGATGGATCAGACGCACCGCTCTTCACCTTGAAGCCTGGAAAGACTTACAGGGTTAGGATCTGTA
K S G K G D G S D A P L F T L K P G K T Y R V R I C N
892 ACGTGGGTGTCAAGACATCTATCAACTTTAGGATTCAGAATCACAAGATGAAGCTCGTTGAAATGGAAGGATCCGCACGTT
V G V K T S I N F R I Q N H K M K L V E M E G S H V
972 CTTCAAAACGATTACGACTCTCTTGACGTTCACGTTGGCCAGTGCTTTGGCACCATCGTTACCGCGAATCAAGAACCTAA
L Q N D Y D S L D V E V G Q C F G T I V T A N Q E P K
1052 AGATTACTACATGGTTGCATCCTCTAGGTTCTTGAAGACGGTTATCACAACAACCGGACTTCTCCGCTACGAGGGAGGCA
D Y Y M V A S S R F L K T V I T T T G L L R Y E G G K
1132 AAGGACCCGCCTCTTCACAGCTTCCGGCTGGTCCGGTCGGATGGGCCTGGTCGTTGAACCAGTTCCGATCCTTCAGGTGG
G P A S S Q L P A G P V G W A W S L N Q F R S F R W

FIG. 3B(3)

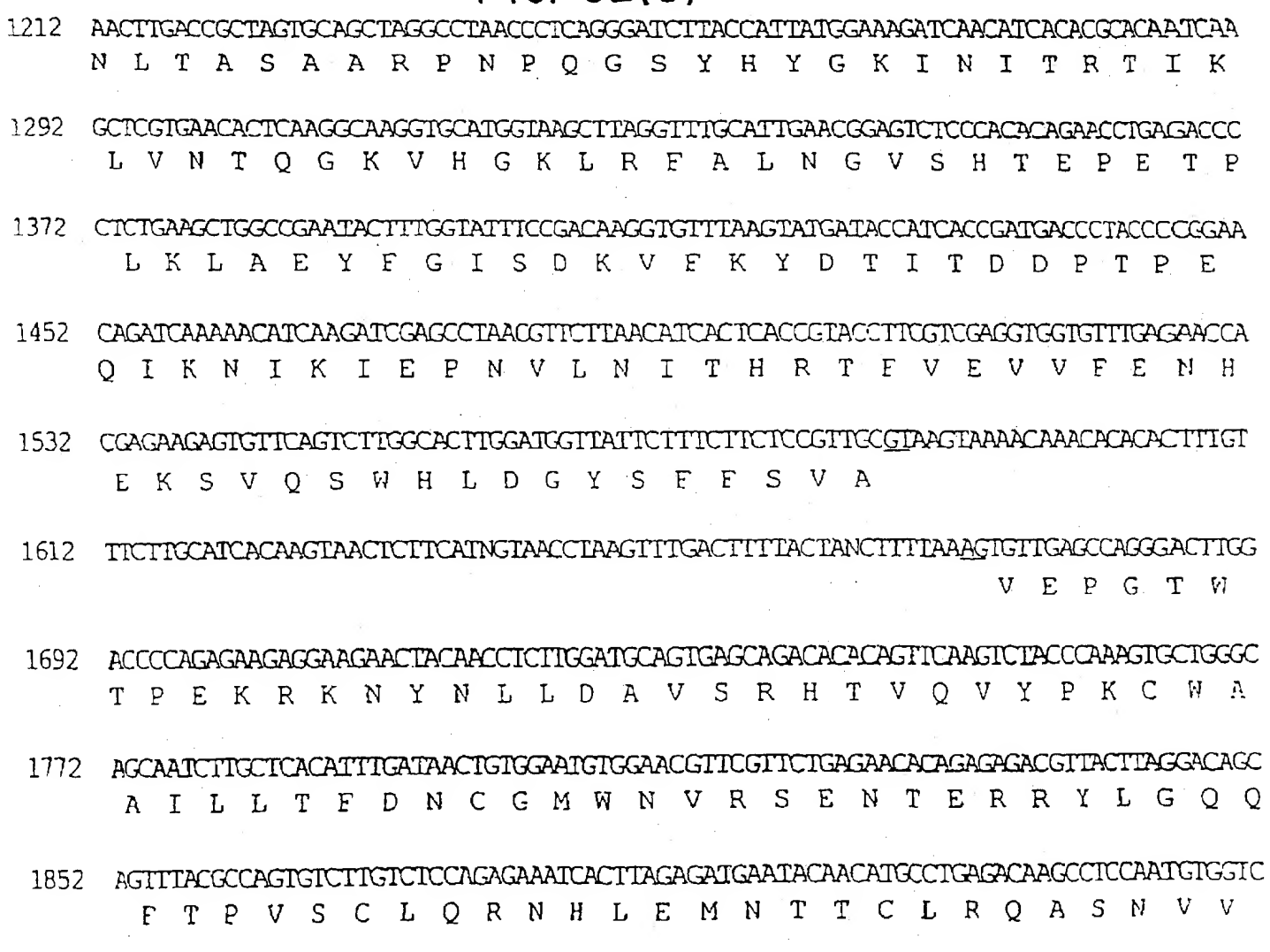

1212 AACTTGACCGCTAGTGCAGCTAGGCCTAACCCTCAGGGATCTTACCATTATGGAAAGATCAACATCACACGCACAATCAA
N L T A S A A R P N P Q G S Y H Y G K I N I T R T I K
1292 GCTCGTGAACACTCAAGGCAAGGTGCATGGTAAGCTTAGGTTTGCATTGAACGGAGTCTCCCACACAGAACCTGAGACCC
L V N T Q G K V H G K L R F A L N G V S H T E P E T P
1372 CTCTGAAGCTGGCCGAATACTTTGGTATTTCCGACAAGGTGTTTAAGTATGATACCATCACCGATGACCCTACCCCGGAA
L K L A E Y F G I S D K V F K Y D T I T D D P T P E
1452 CAGATCAAAAACATCAAGATCGAGCCTAACGTTCTTAACATCACTCACCGTACCTTCGTCGAGGTGGTGTTTGAGAACCA
Q I K N I K I E P N V L N I T H R T F V E V V F E N H
1532 CGAGAAGAGTGTTCAGTCTTGGCACTTGGATGGTTATTCTTTCTTCTCCGTTGCGTAAGTAAAACAAACACACTTTGT
E K S V Q S W H L D G Y S F F S V A
1612 TTCTTGCATCACAAGTAACTCTTCATNGTAACCTAAGTTTGACTTTTACTANCTTTTAAAGTGTTGAGCCAGGGACTTGG
V E P G T W
1692 ACCCCAGAGAAGAGGAAGAACTACAACCTCTTGGATGCAGTGAGCAGACACACAGTTCAAGTCTACCCAAAGTGCTGGGC
T P E K R K N Y N L L D A V S R H T V Q V Y P K C W A
1772 AGCAATCTTGCTCACATTTGATAACTGTGGAATGTGGAACGTTCGTTCTGAGAACACAGAGAGACGTTACTTAGGACAGC
A I L L T F D N C G M W N V R S E N T E R R Y L G Q Q
1852 AGTTTACGCCAGTGTCTTGTCTCCAGAGAAATCACTTAGAGATGAATACAACATGCCTGAGACAAGCCTCCAATGTGGTC
F T P V S C L Q R N H L E M N T T C L R Q A S N V V

FIG. 3B(4)

```
1932  TCGTCAAAAACACACCTAAACCTGTTAACCCTTACGCTGGTGCCTAAGTTTAACTTTTAAATACAACTAAAGAGTTNTGA
      S  S  K  T  H  L  N  L  L  T  L  T  L  V  P  K  F  N  F  *

2012  NTCTTCTGTTGATNTGAAAATTAATTNCTAAAATTATATGGTTTACTCGTATATACATGGAANTGAAAATGTATGTATGT
2092  GTCTATACCTTTTAAGTAATTTTTCTTTCTTTCAAGAAGCATTAGTCTTCTCTTTGTTTTTTGTTCTTCACTTTTTTGTA
2172  ACAATTATGTAATGTATTATGTATCCGATAATCTTCGATGAAATAAGCAAAGAGATCTTATTTCTCCCAAAAAAAAAACT
2252  TTACAATAAAAGTATTTCTCTATAGCCTAGAACCATGTATGATGATAACAAAACCCTTCTTCTTAGTCTGAGCCTTTTTC
2332  TAAGGCTCTTTATCTCGTGGTTCTTCCACCAACGGNGTTTCCTTGAGAGAGAAGTCATCGAGGCTATCATCATTCTCTGT
2412  ATCGACCTGAACAAACTCTTTGAACATCGCCATTACTTGAATCATAGTTGGTCTTTTGAACGGTCGATCGTCCAGACACT
2492  GAGACGCAATCTTCAAGTAATGAAACAGCTCAACGTCGCCAGATTTCTCAGTTATCAGGTCCGAATCAAGAATCTCAGCT
2572  CCTCTACTCTCCTTATAAAGCTGTTTAGCCCATCCCACGAGATTGTTGTCCTCACCAAACTCCTCTGGATCGATCGGTTT
2652  CTTCCCCCAGACAACCTCCACAAGTATAACCCCCTACCTATACACATCTCCTTTCGTCGTCCACCTGAAACTCTCGTAAT
2732  ACTCTGGCGGAACGTAACCGGGAGTTCCCGCGAGCGTGTCACGCTCAAATGCGTGTCCAGAGCGCTCACCAGCCTTGCCA
2812  TACCGAAGTCCGAGACGCGTGCTGTGAAGTCTTGGTCTAGA  2852
```

FIG. 3C(1)

```
1   GAATTCCTCAACANNTGATTCTCATCAACGGACAGTTCCCTGGTCCTAACCTAAACTCCACATCCAACAACAATGTCGTC
      I  P  Q  X  X  I  L  I  N  G  Q  F  P  G  P  N  L  N  S  T  S  N  N  N  V  V

81  ATCAATGTTTTCAACAACCTTGACGAGCCTTTCCTCTTGACCTGGTTAGTCACCATTTCCTCTCATTTTATAGGCATTCT
      I  N  V  F  N  N  L  D  E  P  F  L  L  T  W

161 GTTTCTAAAATTTAAATGATATTTTAAAGCTACAATTTTTTTTTCATTTTTAATATAACTGTTCTTTTACAAAGGCCAAA
241 CGAGAAATGCAAATGGAAAGTTCTCATTTCGTTTGATATTTTCATTTACAGTTAACATATGATTTTTTTTTTCAGATCTT
321 TGTAGGTTTGTTTGAAAAAAGTTTTGGTATAGTTATGTTATTTTGTTTCCTGGATCTTAGGTTTGAATAATTCATAACCA
401 AATTGAAAACAAAAACTTTTGGATCGTTAATCAAATCTTCTTCTTATTTTTTAAATGTTATATTAATTTCACATAATTAC
481 ATCTATATATAATATATAAATACAAATAAAATGATAATTTCAGTTTATCATATATTAAATCAGACTAAAATAATAAAAAC
561 AAAAAGAAATTTAAACACATTTTGACTCAGTTTTAGATTAAGATTGGTTATATTACCACAAGTAATTATGCTAGTCTTCA
641 TTGCAAATTTAAACACATTTTAACTATGTGGGTTCGGTGACATGGCAGGAGTGGTCTCCAGCACAGGAAGAACTCATGGC
                                                    S  G  L  Q  H  R  K  N  S  W  Q

721 AAGATGGTGTGACCGGAACCTCATGCCCAATCCCAGCAGGCACCAACTACACTTACCATTTCCAGCCTAAGGACCAGATC
      D  G  V  T  G  T  S  C  P  I  P  A  G  T  N  Y  T  Y  H  F  Q  P  K  D  Q  I

801 GGTAGCTACTTCTACTACCCATCAACCGCCCTGCACCGTTTCTCCGGTGGTTTCGGTGGCCTCCGTGTCAACAGCCGTCT
      G  S  Y  F  Y  Y  P  S  T  A  L  H  R  F  S  G  G  F  G  G  L  R  V  N  S  R  L

881 CCTCATCCCCNTCCCTTACGCTGACCCCGAAGATGACCACACCATCCTCATCAACGACTGGTACAGCAAGAGCCACACCG
      L  I  P  X  P  Y  A  D  P  E  D  D  H  T  I  L  I  N  D  W  Y  T  K  S  H  T  A

961 CTCTCAAGACCTTCCTTGACAGCGGCCGCACTCTTGGTTCCCCTGACGGTGTCCTCATCAACGGAAAGTCCGGTAAAGTC
      L  K  T  F  L  D  S  G  R  T  L  G  S  P  D  G  V  L  I  N  G  K  S  G  K  V
```

FIG. 3c(2)

```
1041 GGAGGACAAAACAAGCCTCTCTTCACCATGAAGCCAGGAAAGACCTACAAGTACAGAATCTGTAACGTTGGGTTCAAATC
     G  G  Q  N  K  P  L  F  T  M  K  P  G  K  T  Y  K  Y  R  I  C  N  V  G  F  K  S

1121 CACTCTTAACTTCAGGATCCAAGGACACAAGATGAAGCTTGTTGAGATGGAAGGATCTCACGTTCTCCAGAACGACTACG
     T  L  N  F  R  I  Q  G  H  K  M  K  L  V  E  M  E  G  S  H  V  L  Q  N  D  Y  D

1201 ACTCGCTCGACGTCCACGTCGGACAGTCGTTCGCTGTTCTTGTGACCGCTGACCAAGAGGCCAAGAGCTACTACATGGTT
      S  L  D  V  H  V  G  Q  S  F  A  V  L  V  T  A  D  Q  E  A  K  S  Y  Y  M  V

1281 GCATCCACTAGGTTCCTCAAGAAGGAAGTGAGCACTGTTGGTGTGATGAGCTACGAAGGAAGCAATGTTCAGCCTTCAAA
     A  S  T  R  F  L  K  K  E  V  S  T  V  G  V  M  S  Y  E  G  S  N  V  Q  P  S  N

1361 TGTGCTTCCCAAGGCTCCAGTTGGATGGGCTTGGTCTCTTAACCAGTTCAGATCATTCAGATGGAACTTAACCGCCAGCG
     V  L  P  K  A  P  V  G  W  A  W  S  L  N  Q  F  R  S  F  R  W  N  L  T  A  S  A

1441 CGGCTAGGCCTAACCCGCAAGGATCTTACCATTACGGAAAGATCAACATCACACGTACCATCAAGCTCGCCAACACCAAG
      A  R  P  N  P  Q  G  S  Y  H  Y  G  K  I  N  I  T  R  T  I  K  L  A  N  T  K

1521 AACTTGGTGGACGGTAAGGTCAGGTTTGGGCTTAACGGTGTATCACACGTTGACACCNAGACTCCCTTGAAGCTTGCTGA
     N  L  V  D  G  K  V  R  F  G  L  N  G  V  S  H  V  D  T  X  T  P  L  K  L  A  E

1601 GTACTTCNAGATGTCCGAGAAGGTCTTCAAATACAATGTCATCAAGGACGAACCAGCAGCCAAGATCACTACACTAACCG
     Y  F  X  M  S  E  K  V  F  K  Y  N  V  I  K  D  E  P  A  A  K  I  T  T  L  T  V
```

FIG. 3C(3)

```
1681  TTGAGCCTAATGTCCTTAACATCACTTTCCGTACCTTTGTTGAAATCGTCTTCGAGAACCACGAGAAGAGCATGCAATCA
        E  P  N  V  L  N  I  T  F  R  T  F  V  E  I  V  F  E  N  H  E  K  S  M  Q  S

1761  TTCCATTTGGATGGTTACTCCTTCTTCTCAGTCGCGTAAGCTTCATTAATAACTCTATAGGCCAATGTTTCACTTANTAN
        F  H  L  D  G  Y  S  F  F  S  V  A

1841  GCGCAGAACCGGCGTGATCTTTTACTTCAGATATAAGATTCCTAACAATTTTTTTAATATTTTTTCAACAGTTCTGAGCC
                                                                        S  E  P

1921  AGGAACATGGACACCAGAGAAGAGAAACAACTACAACTTGCTCGATGCGGTCAGCAGACACACCGTGCAAGTNTTCCCCA
        G  T  W  T  P  E  K  R  N  N  Y  N  L  L  D  A  V  S  R  H  T  V  Q  V  F  P  K

2001  AGTCGTGGTCCGCCATCCTCTTGACATTCGACAACGCCGGTATGTGGAACATCAGATCAGAGAACTGGGAGAGAAGATAC
        S  W  S  A  I  L  L  T  F  D  N  A  G  M  W  N  I  R  S  E  N  W  E  R  R  Y

2081  TTGGGACAGCAAATGTACGTCAGTGTTCTTTCCCCTGAGAAATCACTAAGAGACGAATACAACATCCCACTCAACACCAA
        L  G  Q  Q  M  Y  V  S  V  L  S  P  E  K  S  L  R  D  E  Y  N  I  P  L  N  T  N

2161  CCTTTGTGGTATCGTTAAGGGCTTGCCATTACCTACACCCTACACTATTTAATTAAACTCACTTCCACAAAAGTTTTATT
        L  C  G  I  V  K  G  L  P  L  P  T  P  Y  T  I  *

2241  TATTTATTTGATATATGTAAAATTCTACTTTTTACAAGTGAGTGTATTACGTGACTAATTAACCCTTTCCTAATTTCATT
```

FIG. 3c(4)

321 TAACATACTACTACTATAATTACAGATCCCATTGTTGTTTCACTAATAGTAATATATACAACATTTAGCTTACTTAATAT
401 AATCCTGATTCTAACACAAAAGACTGTTATTCATTTCATAATGAACAAAACTTGTTCACCCCCTATGGTGAACCCTCTAA
481 TTCACCTCTATTCTTAACACCAATCAAATTGACATGTAAGATTAATAAAAAAAGAAATAAAATTTAAAAGAAAAAAATAG
561 GTTTCCTAAAAAAGGGTTTATTTGTCAAATAACCAAAAAAAAAATGAAAATTANATTTTGGGAGAGAGAGTAGAGAGAGAT
641 AGGAANAAAAAGTAGGAGAGAGGAGAGAATTTTAGTTAGTTAGTGTATTTAAGTTTTTTTCATGTATATAGGGTGCAATT
721 TCCCAAAAAAAAAAGTCTCGGTTAACAAGGAAAATAACGTGTGTTTTGTTACGCCGTCCATCGACGTCTTCTTCTTTATA
801 GCCCAGAGAAGATAGAAAGCTGAGTCTCCAGTTCTATGCTTCCAAATCAAATTTCGATTTCATCTTCTCCAAATCAAATC
881 AAGCCATGTTGCCTTATGAGTAGAAAGAGCGCTGATGGTGGAGATGAAGATGATGGTATGGGATTCAAACTTGCAGGCCC
961 CAGGGAGGAAGAAGATGACTTTACTTGTGAACCAGNCTGTGCCTAAAATTCAACAAAAGAAACCGATGGCAATTGGAAAT
1041 CAGACACTACAACTTGNTTAAATAAAAACGCTANTTGTAATGTATTCTTAGAATATAGACTTGCAAGTTGATGAGAACTC
1121 ACTGATGCAAGTGTCGTGATCTTTGATGTAGTAAGGTCACAGCAACAGACTTTTAATGTATTCTTAAAATATAGATTTGC
1201 AAGTTCTTTGTTGTATTTCTTCTTCTTCGTGGGACATCTGACCTGTAAATCAGAGATATAATCCCACCAAACCCAAGGTT
1281 TCCTGGTTTAATT 3293

FIG. 3D(1)


-2022 GGATCCGTTCCTTTCCGGTCATTTTCTCTCTCCGTCCATAGGAGAACATCCGATCATGATCACTCCGATCAAACTAGCCT
-1942 TTCTCTTATTATTCATCACCACAACAGCAACCGCTGCACCCAAAGCCAAACGCAGGAACTACCTTTTCACACCGCATGCA
-1862 AAAGCAGTCGCGGAATATGCACTGTTGTCCTAACAAACACAAGTCCATGCTGTAAAACCCTTAAACACGTTCCTACCGAT
-1782 GACCCTATCGAATTGATCCGAGCGTTAGCGGCTGCGACTGAATCTTCTGTGAAAAGAAGTGTGGTTTTCCTCTCCGAGAT
-1702 CAAACCAAAACACAAATCAAACGCAACCGCAGCTGCAGTGGTCAACAGCTGCGAAAAAAACTTGAAGTACGCATTAGAAG
-1622 ATTTCACTGATTTTTGGAACGCTATGCGGAAAGATGTAAAGACGTTGGCTCATAACTATTTCACGTGTAAGAAGAAGTTA
-1542 ATGTCGATCATGGGGTACCATTGGACTTGTTTGGATGATATTGATGATAAGAATCTGTTGAAGGAANTGGAGACTGGGAT
-1462 TAGTGTTGCGAAGAATCTAAGCAGTAATACGTATGATGTGTTTAATGGTTTGAAAACTATTTTTAAGACGTTTGGTATCA
-1382 AGGTGAAACTTAACGAGGAAGACACTTCGCCCCAACCGCCACCATTGTCGAATTATTACTACTGATTAAATGATTTGGAT
-1302 GTAATAAATAATTAATATCACTCGTATAATGCCTAAAGCGACCATATATGTACGATGTATGTTCTAGGTTTTATACATGT
-1222 ACGGATGGATTTCGAGATGATTGGAAAGGATATATTAATGGAATGTGAGTTTTTTTATAAGTTTTTGAATTGTCATCAAA
-1142 ATGAACCTGAAAGTATATATGTTGATTACATAATTATTTGATAGACCTTGATAACTCGAACAAATATACTATCGCAATCA
-1062 TTATTGGTTAAATGTTTTCGGATACATGTCCTACGTCAAACAAAATAATTGTGCATTTTTCATATATTTGATGCATGAAA
-982 GTTTCATATATTTGATGATGAAACCATGCATTTGTTTCCTTGTGCTCCCGGGACTTGTCAACATTCAACGAACCTTCAGT
-902 AATCAACTACATATGATACTGATCTAGATGATGTATGTACATGTACGACCATGCATGAATCACGCCGATGTTTCTTTTAT
-822 CAAGGCGATGTTTAAAATGTACCCCGCTTTCTCGTTCTGGTAGGTATAAATACGAGTGAAATAACATTCCTATGTATAGT
-742 ATAGTAGTTCATTTTGTTGACCAAAATTTAAATATATAGGACATAATTATATTTTCTCAAATGAATTTGAGTTTTGAGTG
-662 CCTCCTGAAAAGATGATTCCAGCTTTCAATTTTACAATGCTGGGTCAACCCCCCCCAAGTATTATCGTTATAAAAAAATAC
-582 TCAGAATAATCTCACACCTAAAACTGCGCATGAACTTGTTAATAGTCTAAAAAGATGTCCATGAACTGAATGAATAATAC
-502 CATTCATGTTTGAGTAACACCATAGATGACACAATTTTCTTACTACCACTAATAGATGACACAATTGTCTTTGTTACATG
-422 TTGTAGTGTCCGATTAATTTGGGTTGAAGAAGATGAGAACTCTCGATGAGAAGCTTTAGAAACATGCATTTACTTTCGTT
-342 ACTTTCGAAATTCGGATGTAAAACTAGTACTAGGAATGAAAATCCCAAAATAAGTTGTTTATTCTCTCTAATCCTAAAAT
-262 TAATAAAATTATAATAGACTAACTTTTCCATCCTTAAGTTACTTCTTATTTTTAGTAATCGAAGCTACACCTCTTGATCA
-182 GGACAAAGACATAATCAAATCATCTTGTGGTGAATAATTTTTAATCTCAAATCCAATATTTGATTAGAGAAGTTTCAGCC

FIG. 3D(2)


-102 ATTCAACTACCTAAAATGTCTCCCTCCATGCAAAGCTCATGCGAACCTAATTTTAGAAACTACAACTTCTATAAGAATCT
-22 CCCATAATGCACCATAATCTCCACCAGCCCCCATTAAATAATCCACCGGGTCTGAATAAATAAAAATAAGTCCCCTCCCT
59 CTCCTATTTACCTCCTAAATAAAACCTGAGGGAGAAAAAACAAAAAAAAAACAAAAAAATAGATTAAAAAATAAATAATG
M
139 GCGGTCGGGAAAATTGTGATATCAGTGGCATCCATGCTTCTAGTGGTGGGTGTTGCCATAGGAGTTGTCACCTTTGTTAA
A V G K I V I S V A S M L L V V G V A I G V V T F V N
219 TAAAGGTGGTGGTGCAGGTGGCGACAAGACTCTGAACTCGCATCAGAAAGCGGTTGAGTCACTTTGTGCGTCAGCCACAG
K G G G A G G D K T L N S H Q K A V E S L C A S A T D
299 ACAAAGGTTCATGCGCAAAAACACTTGACCCAGTCAAAAGCGACGATCCAAGTAAACTTATCAAAGCCTTCATGTTAGCT
K G S C A K T L D P V K S D D P S K L I K A F M L A
379 ACAAAAGATGCTGTCACAAAATCCACAAACTTCACGGCTTCAACCGAAGAAGGTATGGGGAAAAACATTAACGCGACGAG
T K D A V T K S T N F T A S T E E G M G K N I N A T S
459 CAAAGCCGTTCTTGATTACTGCAAGAGAGTGCTGATGTACGCTCTCGAGGATCTTGAGACCATTGTTGAAGAAATGGGTG
K A V L D Y C K R V L M Y A L E D L E T I V E E M G E
539 AAGATCTTCAGCAGAGTGGGAGTAAGATGGACCAGCTTAAACAATGGTTAACCGGAGTTTTTTAATTACCAAACCGATTGT
D L Q Q S G S K M D Q L K Q W L T G V F N Y Q T D C
619 ATTGATGATATTGAAGAATCGGAACTAAGAAAAGTCATGGGCGAAGGAATCGCTCACTCCAAGATTTTGTCCAGTAACGC
I D D I E E S E L R K V M G E G I A H S K I L S S N A

FIG. 3D(3)

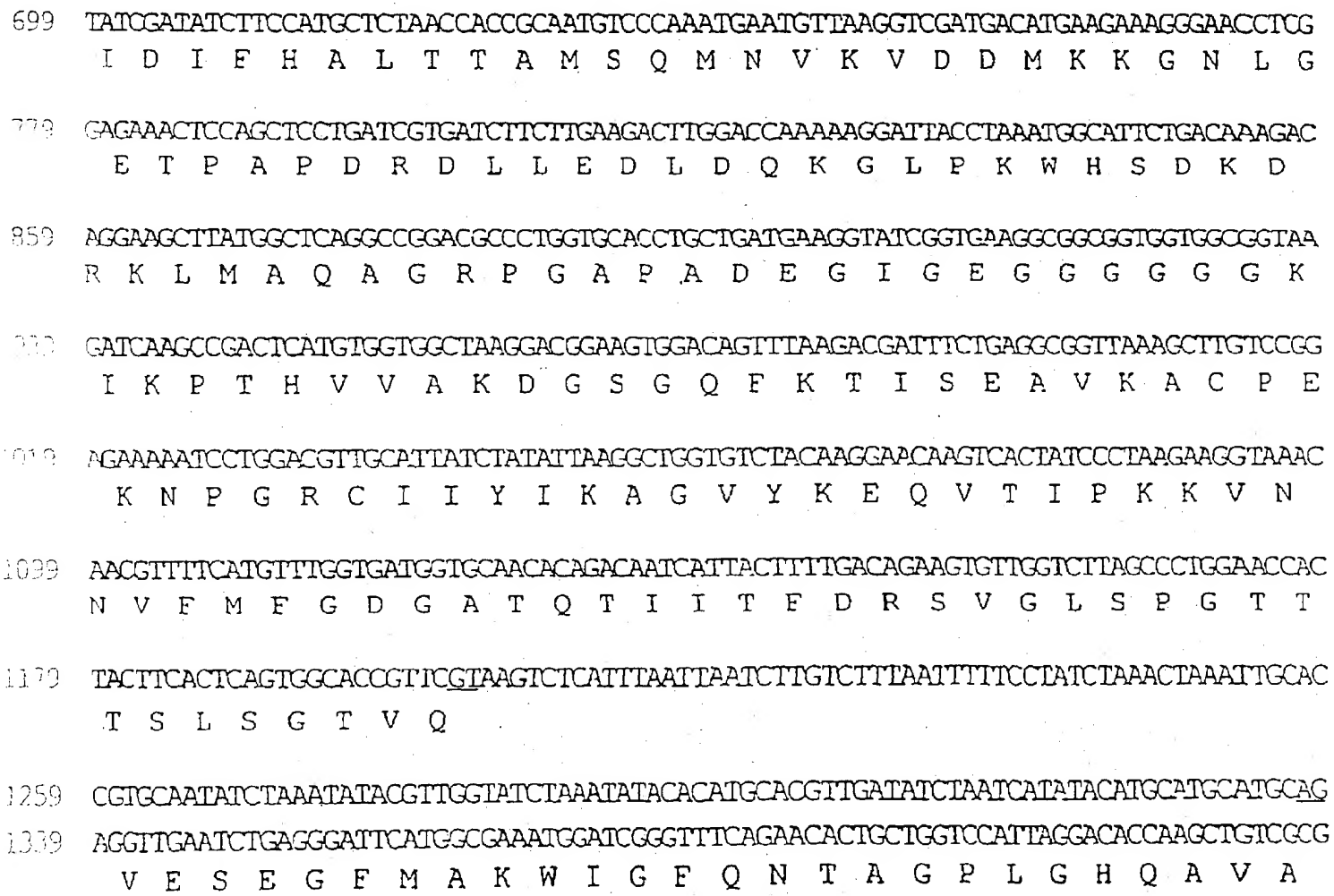

699 TATCGATATCTTCCATGCTCTAACCACCGCAATGTCCCAAATGAATGTTAAGGTCGATGACATGAAGAAAGGGAACCTCG
I D I F H A L T T A M S Q M N V K V D D M K K G N L G
779 GAGAAACTCCAGCTCCTGATCGTGATCTTCTTGAAGACTTGGACCAAAAAGGATTACCTAAATGGCATTCTGACAAAGAC
E T P A P D R D L L E D L D Q K G L P K W H S D K D
859 AGGAAGCTTATGGCTCAGGCCGGACGCCCTGGTGCACCTGCTGATGAAGGTATCGGTGAAGGCGGCGGTGGTGGCGGTAA
R K L M A Q A G R P G A P A D E G I G E G G G G G G K
939 GATCAAGCCGACTCATGTGGTGGCTAAGGACGGAAGTGGACAGTTTAAGACGATTTCTGAGGCGGTTAAAGCTTGTCCGG
I K P T H V V A K D G S G Q F K T I S E A V K A C P E
1019 AGAAAAATCCTGGACGTTGCATTATCTATATTAAGGCTGGTGTCTACAAGGAACAAGTCACTATCCCTAAGAAGGTAAAC
K N P G R C I I Y I K A G V Y K E Q V T I P K K V N
1099 AACGTTTTCATGTTTGGTGATGGTGCAACACAGACAATCATTACTTTTGACAGAAGTGTTGGTCTTAGCCCTGGAACCAC
N V F M F G D G A T Q T I I T F D R S V G L S P G T T
1179 TACTTCACTCAGTGGCACCGTTCGTAAGTCTCATTTAATTAATCTTGTCTTTAATTTTTCCTATCTAAACTAAATTGCAC
T S L S G T V Q
1259 CGTGCAATATCTAAATATACGTTGGTATCTAAATATACACATGCACGTTGATATCTAATCATATACATGCATGCATGCAG
1339 AGGTTGAATCTGAGGGATTCATGGCGAAAATGGATCGGGTTTCAGAACACTGCTGGTCCATTAGGACACCAAGCTGTCGCG
V E S E G F M A K W I G F Q N T A G P L G H Q A V A

FIG. 3D(4)

```
1419  TTCCGTGTGAACGGAGACCGTGCGGTCATATTCAACTGCAGATTTGACGGTTACCAAGACACGCTCTACGTCAACAACGG
        F  R  V  N  G  D  R  A  V  I  F  N  C  R  F  D  G  Y  Q  D  T  L  Y  V  N  N  G

1499  ACGTCAGTTCTACAGGAACATTGTTGTATCCGGTACAGTCGATTTCATCTTCGGAAAAICTGCGACCGTGATTCAAAACT
        R  Q  F  Y  R  N  I  V  V  S  G  T  V  D  F  I  F  G  K  S  A  T  V  I  Q  N  S

1579  CTCTAATCCTCTGCCGAAAGGGAAGCCCCGGACAAACCAACCACGTCACAGCCGACGGTAACGAGAAGGGTAAAGCGGTG
          L  I  L  C  R  K  G  S  P  G  Q  T  N  H  V  T  A  D  G  N  E  K  G  K  A  V

1659  AAGATTGGTATCGTTCTCCATAACTGCCGTATCATGGCGGACAAAGAGCTCGAAGCTGACAGGCTAACCGTCAAATCATA
        K  I  G  I  V  L  H  N  C  R  I  M  A  D  K  E  L  E  A  D  R  L  T  V  K  S  Y

1739  CCTTGGACGGCCGTGGAAACCATTTGCCACCACCGCAGTTATCGGAACTGAGATTGGCGATTTGATTCAACCGACAGGAT
        L  G  R  P  W  K  P  F  A  T  T  A  V  I  G  T  E  I  G  D  L  I  Q  P  T  G  W

1819  GGAACGAATGGCAAGGAGAAAAATTCCATTTGACAGCTACATATGTTGAGTTCAATAACCGTGGACCAGGAGCTAACACT
          N  E  W  Q  G  E  K  F  H  L  T  A  T  Y  V  E  F  N  N  R  G  P  G  A  N  T

1899  GCTGCGAGGGTTCCTTGGGCTAAGATGGCTAAGTCTGCTGCTGAGGTTGAACGTTTCACCGTCGCTAACTGGTTGACTCC
        A  A  R  V  P  W  A  K  M  A  K  S  A  A  E  V  E  R  F  T  V  A  N  W  L  T  P

1979  TGCTAACTGGATTCAAGAAGCCAACGTTCCTGTCCAGCTTGGATTATAAGAAAACTAACTAACAAAATATATAACGAATA
        A  N  W  I  Q  E  A  N  V  P  V  Q  L  G  L  *

2059  ATATATAGTATGTGATCATGTAAAAAGGTAACGATACGACCTCGTCTCTCGGGATCAGGGCTCTTTTTGGTTATTATTAG
```

FIG. 3D(5)

2139 GGTTCTAGGCGTTTTGGGATGATGTTTGTATAAGATTGCTTTTGTTTCACATGCAAAACATATATACAAAATATCTTATT
2219 TCTTCTTTTACTTTCTTTTATTCAAAATAATGAGTTTTTATAACCATGTTGATCTCTATATTATAGACATCCTATCCCTA
2299 AACATGATAAATATAACTTCAAACTAATACCCTAGTAAAAATATATAAACAAAAAAATACTTATGTAAGATTATGTGCAA
2379 GCATGGCTCAACAAATATAACTTTATAAAAAGTTTGCATTATTGCTATGTTTATATATGATTGCTATATGTAAGTATGTT
2459 GATAGAAGTTTATGAGGACAGAGATGACTATTGGCAAATATTAATGAGAAGTGTGATATGTTATCATTTATCAAAACAAA
2539 GCAAGCCCTATATTACCAAATCAAATCTCACTTCAAAGCGAAGCTGCCCATTGATGATCTCACCAATATTTCACACATTA
2619 CAAACGTGACATTATCTTCTCTTCTATGGCTGTTTCCTTAACCAAAGTAAACAGAGTCCAAATCCAACCTTCCAAACCAA
2699 CCCCATTCATCTTATTGGGATCTGTCCTTGATCGATAACATTCCGGTTTTAAGATGTTTCGCAAGGACAATACATCTCTT
2779 TACGCATGGACCTGATGCTGCTAGTAGAGTCATAAAAGATGCATCGGCTAAAGCAGTTGTCCCTTACTATCAATTGTTAA
2859 AGATCCTAAGGTGCTGCTATTGGATGAAGCAACAAGTTCCCTAGACGCCTAATCGGACTATGTGGTCCAAGATTCACTGG
2939 ACCGGGTTATGGTTGAC 2955

FIG. 4

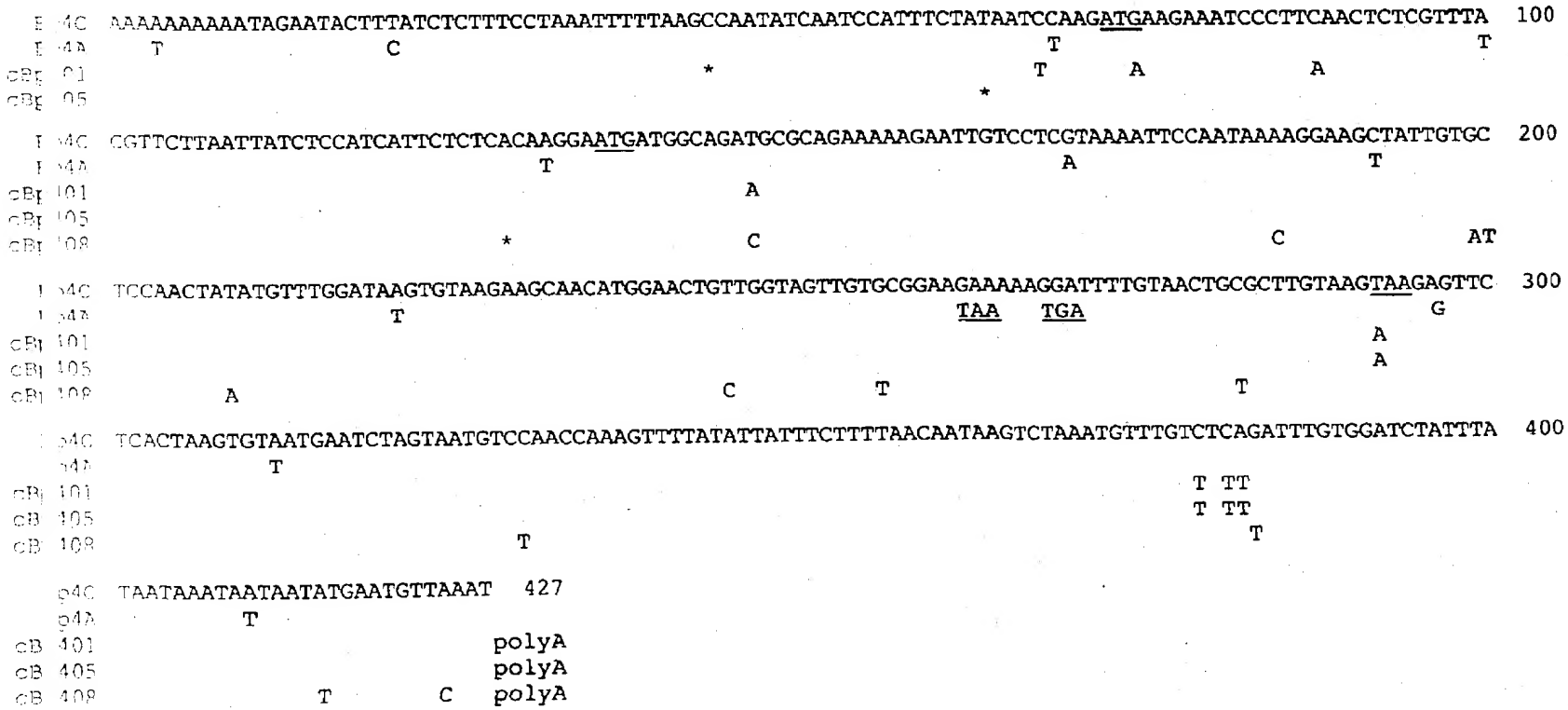

p4C AAAAAAAAAATAGAATACTTTATCTCTTTCCTAAATTTTTAAGCCAATATCAATCCATTTCTATAATCCAAGATGAAGAAATCCCTTCAACTCTCGTTTA 100
p4A T C T T
cB1 101 * T A A
cB1 105 *
p4C CGTTCTTAATTATCTCCATCATTCTCTCACAAGGAATGATGGCAGATGCGCAGAAAAAGAATTGTCCTCGTAAAATTCCAATAAAAGGAAGCTATTGTGC 200
p4A T A T
cB1 101 A
cB1 105
cB1 108 * C C AT
p4C TCCAACTATATGTTTGGATAAGTGTAAGAAGCAACATGGAACTGTTGGTAGTTGTGCGGAAGAAAAAGGATTTTGTAACTGCGCTTGTAAGTAAGAGTTC 300
p4A T TAA TGA G
cB1 101 A
cB1 105 A
cB1 108 A C T T
p4C TCACTAAGTGTAATGAATCTAGTAATGTCCAACCAAAGTTTTATATTATTTCTTTTAACAATAAGTCTAAATGTTTGTCTCAGATTTGTGGATCTATTTA 400
p4A T
cB1 101 T TT
cB1 105 T TT
cB1 108 T T
p4C TAATAAATAATAATATGAATGTTAAAT 427
p4A T
cB1 401 polyA
cB1 405 polyA
cB1 408 T C polyA

FIG. 5

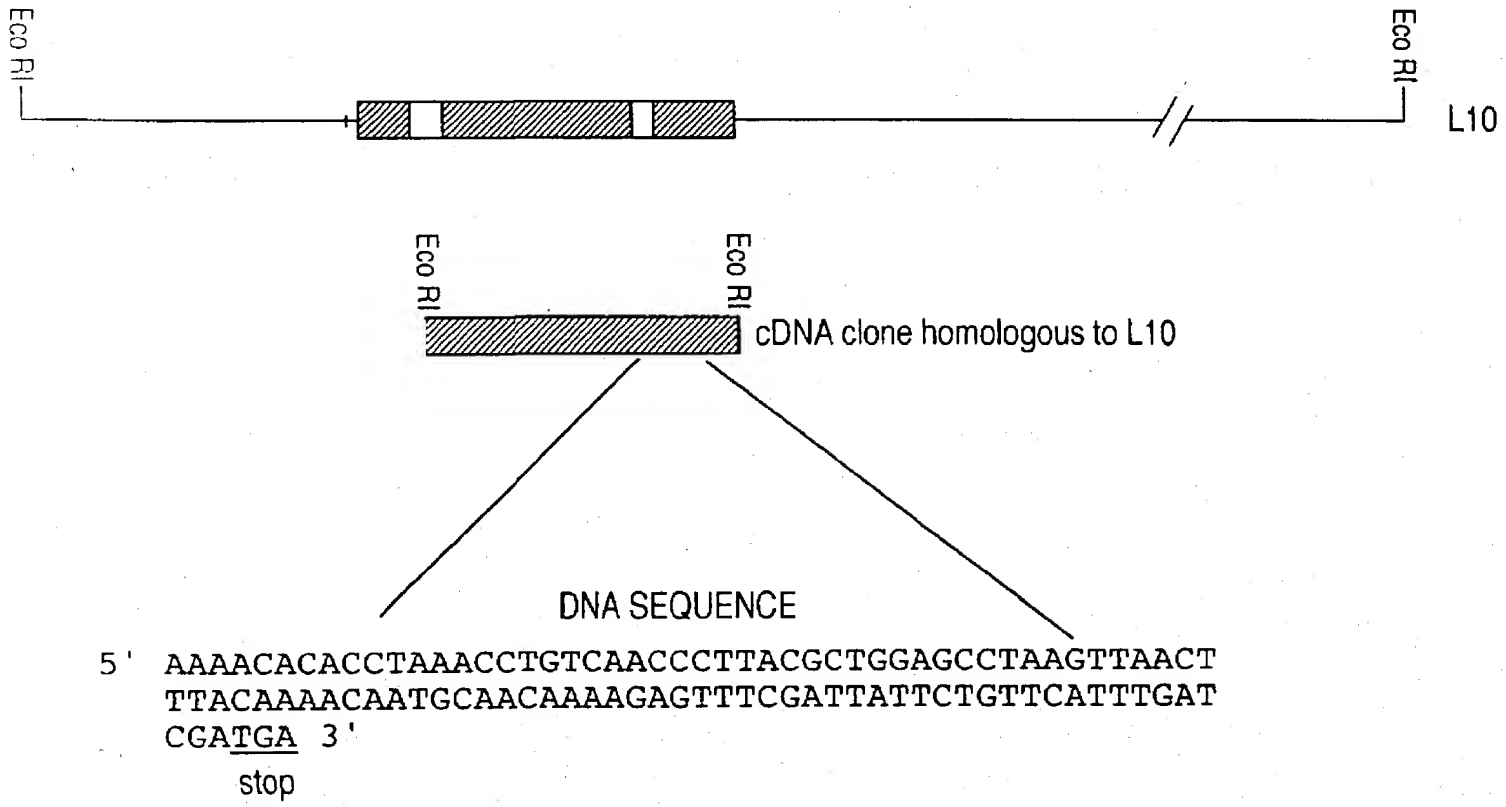

Eco RI
Eco RI
L10
Eco RI
Eco RI
cDNA clone homologous to L10
DNA SEQUENCE
5' AAAACACACCTAAACCTGTCAACCCTTACGCTGGAGCCTAAGTTAACT
TTACAAAACAATGCAACAAAAGAGTTTCGATTATTCTGTTCATTTGAT
CGATGA 3'
stop

FIG. 6

Eco RV

GGAAAATTGTGATATCAGTGGCATCCATGCTTCTAGTGGTGGGTGTTGCCATAGGAGTTGTCACCTTTGTTAATAAAGG
TGGTGGTGCAGGTGGCGAGACTCTGAACTCGCATCAGAAAGCGGTTGAGTCACTTTGTGCGTCAGCCACAGACAAAGGT
TCATGCGCAAAAACACTTGACCCAGTCAAAAGCGATCCAAGTAAACTTATCAAAGCCTTCATGTTAGCTACAAAAGATG
CTGTCACAAAATCCACAAACTTCACGGCTTCAACCGAAGAAGGTATGGGGAAAATTAACGCGACGAGCAAAGCCGTTCT
TGATTACTGCAAGAGAGTGCTGATGTACGCTCTCGAGGATCTTGAGACCATTGTTGAAGAAATGGGTGAAGATCTTCAG
CAGAGTGGGAGTAAGATGGACCAGCTTAAACAATGGTTAACCGGAGTTTTTAATTACCAAACCGATTGTATTGATGATA
TTGAAGAATCGGAACTAAGAAAAGTCATGGGCGAAGGAATCGCTCACTCCAAGATTTTGTCCAGTAACCCTATCGATAT
CTTCCATGCTCTAACCACCGCAATGTCCCAAATGAATGTTAAGGTCGATGACATGAAGAAAGGGAACCTCGGAGAAACT
CCAGCTCCTGATCGTGATCTTCTTGAAGACTTGGACCAAAAAGGATTACCTAAATGGCATTCTGACAAAGACAGGAAGC
TTATGGCTCAGGCCGGACGCCCTGGTGCACCTGCTGATGAAGGTATCGGTGAAGGCGGCGGTGGTGGCGGTAAGATCAA
GCCGACTCATGTGGTGGCTAAGGACGGAAGTGGACAGTTTAAGACGATTTCTGAGGCGGTTAAAGCTTGTCCGGAGAAA
AATCCTGGACGTTGCATTATCTATATTAAGCCTGGTGTCTACAAGGAACAAGTCACTATCCCTAAGAAGGTAAACAACG
TTTTCATGTTTGGTGATGGTGCAACACAGACAATCATTACTTTTGACAGAAGTGTTGGTCTTAGCCCTGGAACCACTAC
TTCACTCAGTGGCACCGTTCGTAAGTCTCATTTAATTAATCTTGTCTTTAATTTTTCCTATCTAAACTAAATTGCACCG
TGCAATATCTAAATATACGTTGGTATCTAAATATACACATGCACGTTGATATCTAATCATATACATGCATGCATGCAGA
CGTTGAATCTGAGCGATTCATGGCGAAATGGATCGGGTTTCAGAACACTGCTGGTCCATTAGGACACCAAGCTGTCGCG
TTCCGTGTGAACGGAGACCGTGCGGTCATATTCAACTGCAGATTTGACGGTTACCAAGACACGCTCTACGTCAACAACG
GACGTCAGTTCTACAGGAACATTGTTGTATCCGGTACAGTCGATTTCATCTTCGGAAAATCTGCGACCGTGATTCAAAA
CTCTCTAATCCTCTGCCGAAAGGGAAGCCCCGGACAAACCAACCACGTCACAGCCGACGGTAACGAGAAGGGTAAAGCG
GTGAAGATTGGTATCGTTCTCCATAACTGCCGTATCATGGCGGACAAAGAGCTCGAAGCTGACAGGCTAACCGTCAAAT
CATACCTTGGACGGCCGTGGAAACCATTTGCCACCACCGCAGTTATCGGAACTGAGATTGGCGATTTGATTCAACCGAC
AGGATGGAACGAATGGCAAGGAGAAAAATTCCATTTGACAGCTACATATGTTGAGTTCAATAACCGTGGACCAGGAGCT
AACACTGCTGCGAGGGTTCCTTGGGCTAAGATGGCTAAGTCTGCTGCTGAGGTTGAACGTTTCACCGTCGCTAACTGGT
TGACTCCTGCTAACTGGATTCAAGAAGCCAACGTTCCTGTCCAGCTTGGATTATAAGAAAACTAACTAACAAAATATAT
AACGAATAATATATAGTATGTGAAAAAAAAAAAAAAAAAAA

FIG. 7A

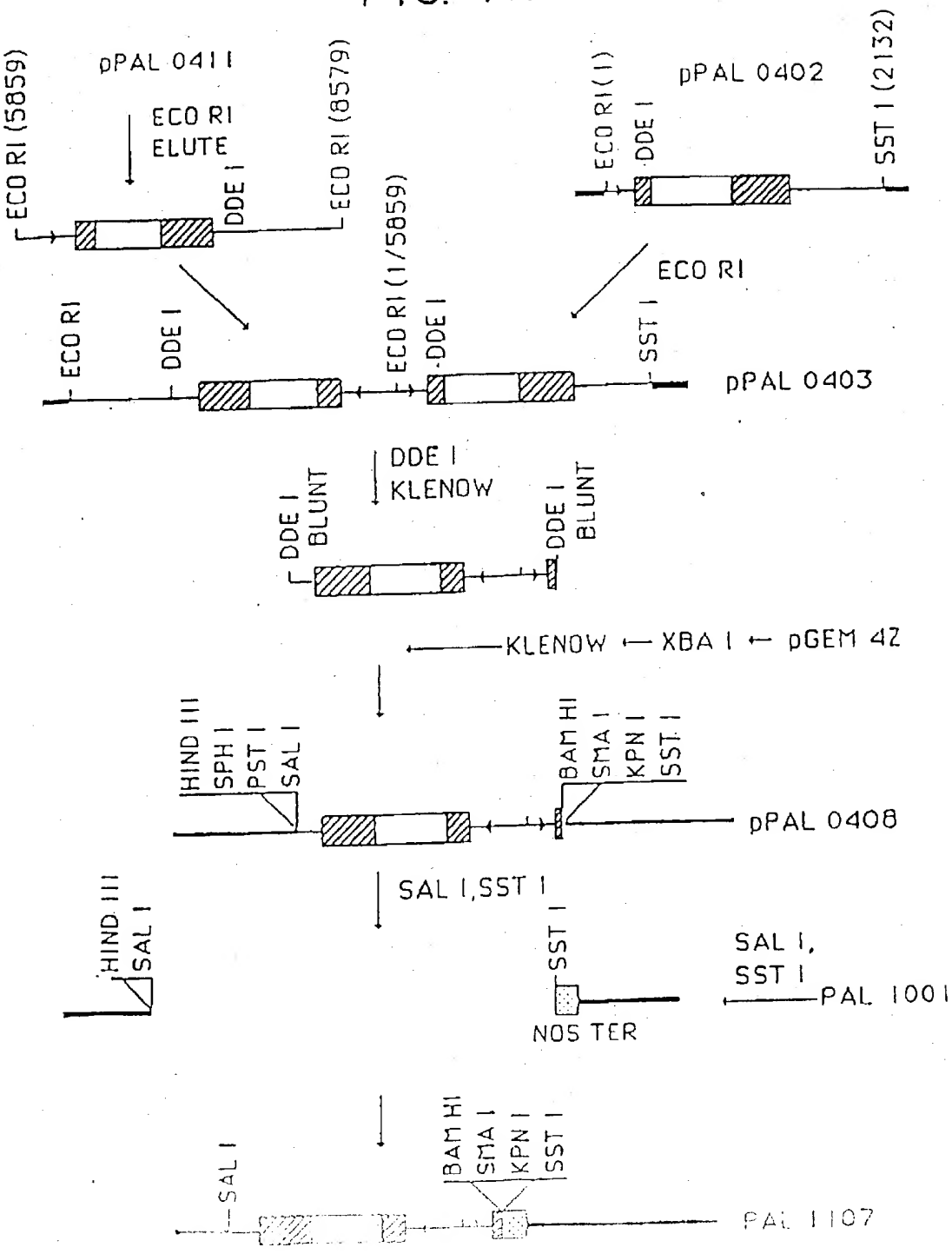

pPAL 0411
ECO RI (5859)
ECO RI ELUTE
DDE I
ECO RI (8579)
pPAL 0402
ECO RI(1)
DDE I
SST I (2132)
ECO RI
ECO RI
DDE I
ECO RI (1/5859)
DDE I
SST I
pPAL 0403
DDE I KLENOW
DDE I BLUNT
DDE I BLUNT
KLENOW ← XBA I ← pGEM 4Z
HIND III
SPH I
PST I
SAL I
BAM HI
SMA I
KPN I
SST I
pPAL 0408
SAL I, SST I
HIND III
SAL I
SST I
SAL I, SST I
PAL 1001
NOS TER
BAM HI
SMA I
KPN I
SST I
SAL I
PAL 1107

FIG. 7B

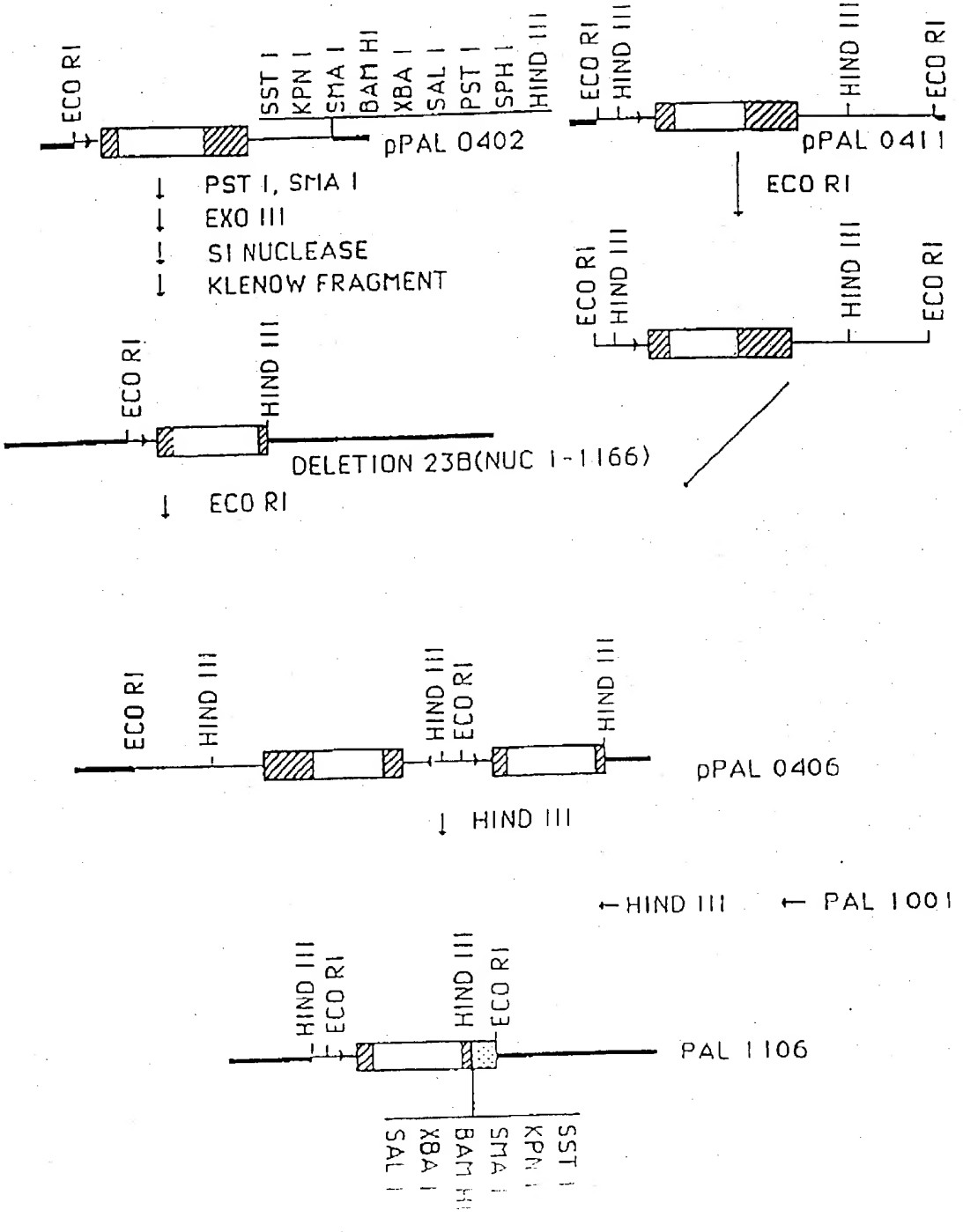

ECO RI
SST I
KPN I
SMA I
BAM HI
XBA I
SAL I
PST I
SPH I
HIND III
pPAL 0402
PST I, SMA I
EXO III
S1 NUCLEASE
KLENOW FRAGMENT
ECO RI
HIND III
DELETION 23B(NUC 1-1166)
ECO RI
pPAL 0411
ECO RI
pPAL 0406
HIND III
HIND III
PAL 1001
PAL 1106

FIG. 7C

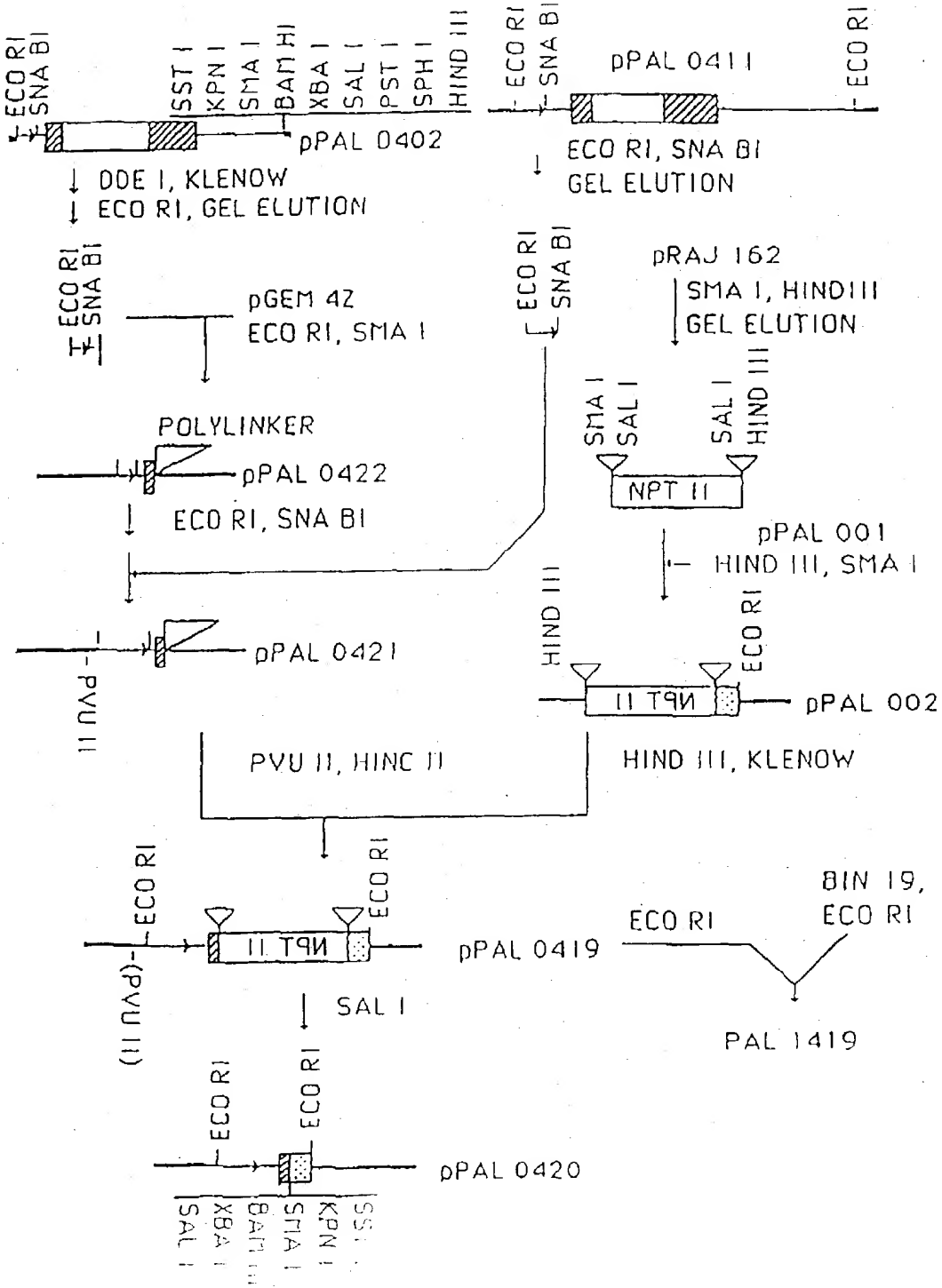

ECO RI
SNA BI
SST I
KPN I
SMA I
BAM HI
XBA I
SAL I
PST I
SPH I
HIND III
pPAL 0402
pPAL 0411
DDE I, KLENOW
ECO RI, GEL ELUTION
ECO RI, SNA BI
GEL ELUTION
pGEM 4Z
pRAJ 162
SMA I, HINDIII
POLYLINKER
pPAL 0422
NPT II
pPAL 001
HIND III, SMA I
pPAL 0421
pPAL 002
PVU II, HINC II
HIND III, KLENOW
BIN 19,
PAL 1419
pPAL 0419
SAL I
pPAL 0420

FIG. 7D

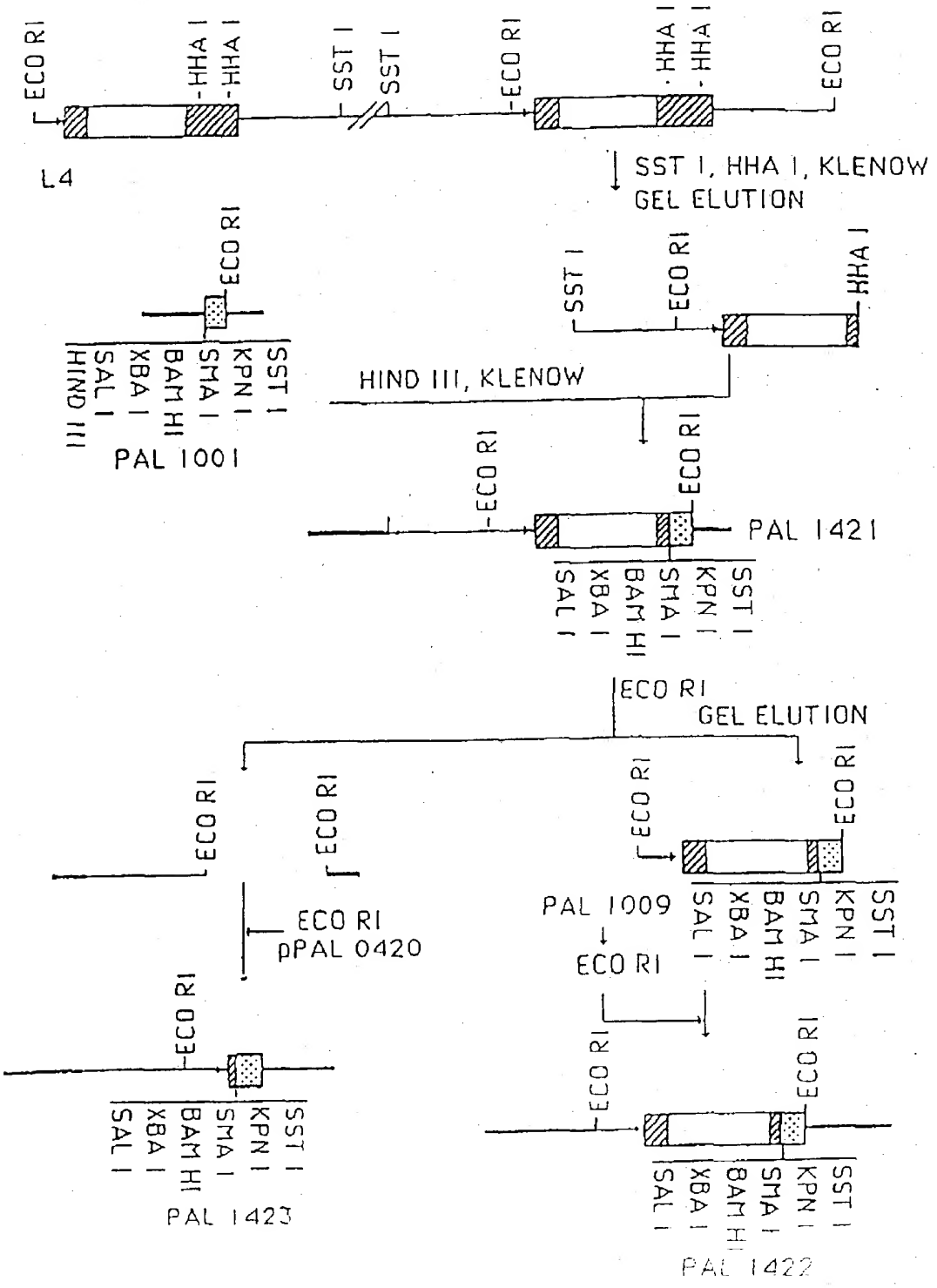

ECO RI
HHA I
HHA I
SST I
SST I
ECO RI
HHA I
HHA I
ECO RI
L4
SST I, HHA I, KLENOW
GEL ELUTION
ECO RI
HIND III
SAL I
XBA I
BAM HI
SMA I
KPN I
SST I
PAL 1001
SST I
ECO RI
HHA I
HIND III, KLENOW
ECO RI
ECO RI
PAL 1421
SAL I
XBA I
BAM HI
SMA I
KPN I
SST I
ECO RI
GEL ELUTION
ECO RI
ECO RI
ECO RI
ECO RI
PAL 1009
SAL I
XBA I
BAM HI
SMA I
KPN I
SST I
ECO RI
pPAL 0420
ECO RI
ECO RI
ECO RI
SAL I
XBA I
BAM HI
SMA I
KPN I
SST I
PAL 1423
ECO RI
ECO RI
SAL I
XBA I
BAM HI
SMA I
KPN I
SST I
PAL 1422

FIG. 7E

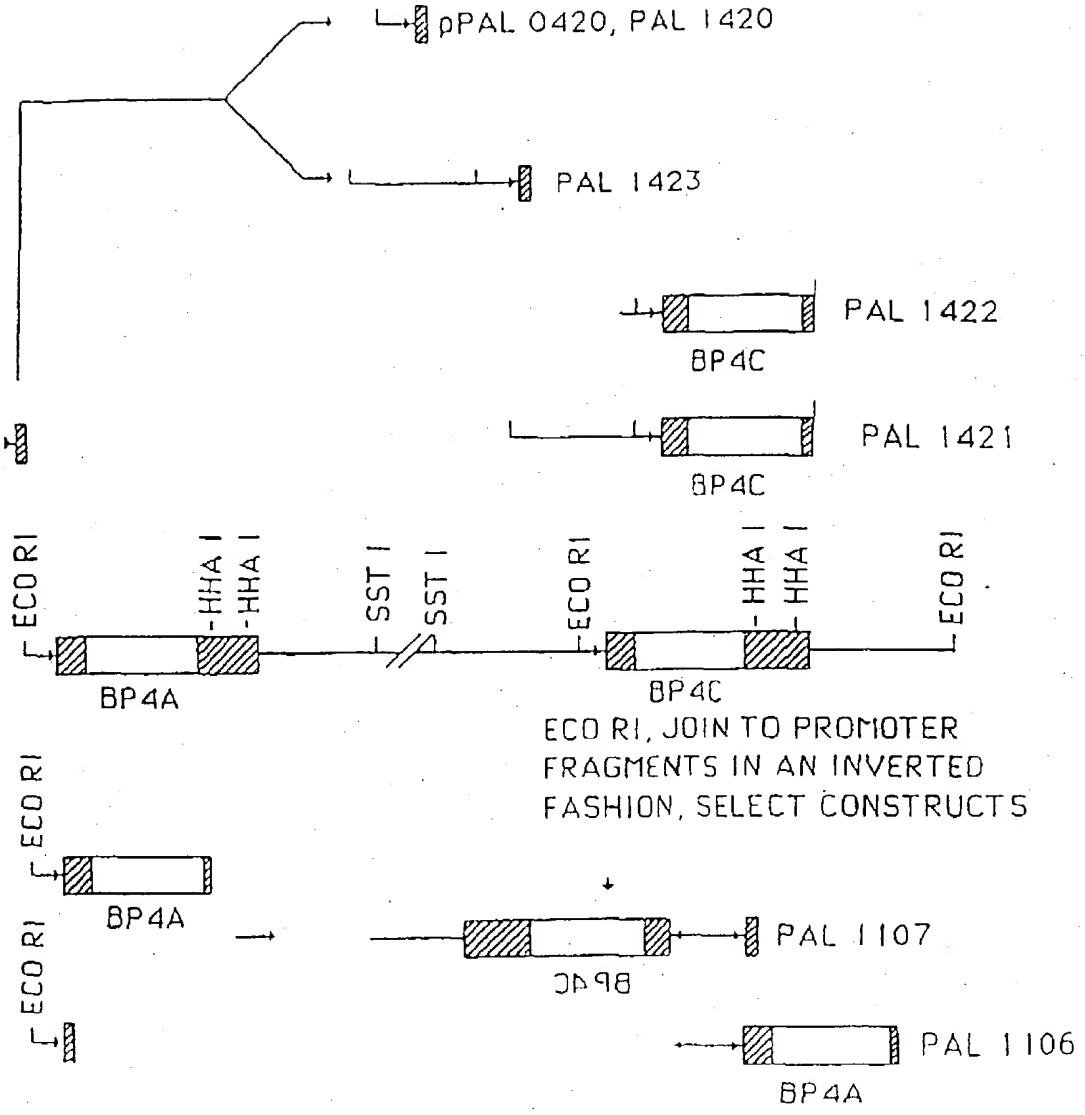
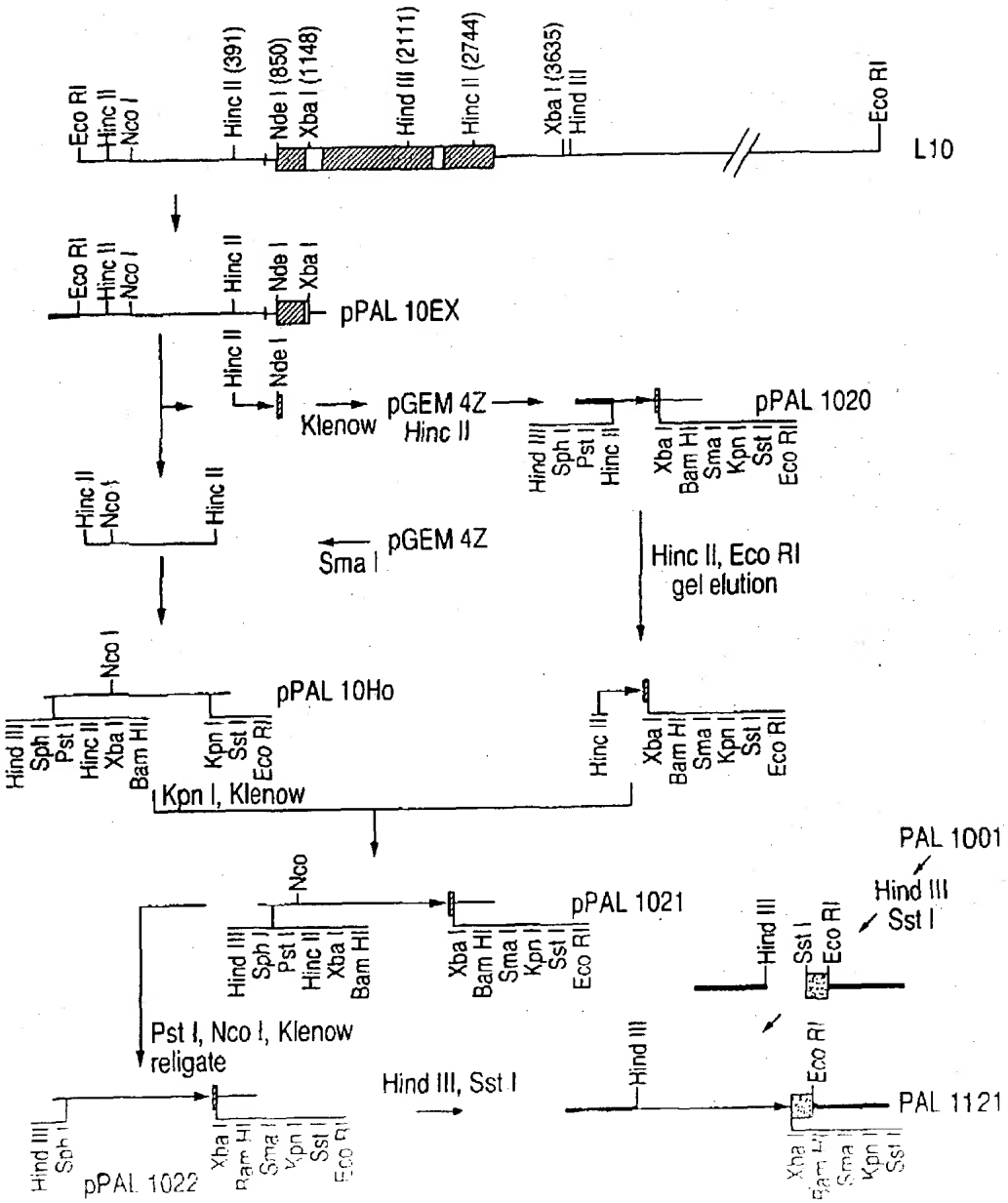

pPAL 0420, PAL 1420
PAL 1423
PAL 1422
BP4C
PAL 1421
BP4C
ECO RI
HHA I
HHA I
SST I
SST I
ECO RI
HHA I
HHA I
ECO RI
BP4A
BP4C
ECO RI, JOIN TO PROMOTER FRAGMENTS IN AN INVERTED FASHION, SELECT CONSTRUCTS
ECO RI
BP4A
ECO RI
PAL 1107
BP4C
ECO RI
PAL 1106
BP4A

FIG. 8


Eco RI
Hinc II
Nco I
Hinc II (391)
Nde I (850)
Xba I (1148)
Hind III (2111)
Hinc II (2744)
Xba I (3635)
Hind III
Eco RI
L10
pPAL 10EX
Klenow
pGEM 4Z
Hinc II
pPAL 1020
Sma I
pGEM 4Z
Hinc II, Eco RI
gel elution
pPAL 10Ho
Kpn I, Klenow
PAL 1001
Hind III
Sst I
pPAL 1021
Pst I, Nco I, Klenow
religate
Hind III, Sst I
pPAL 1022
PAL 1121

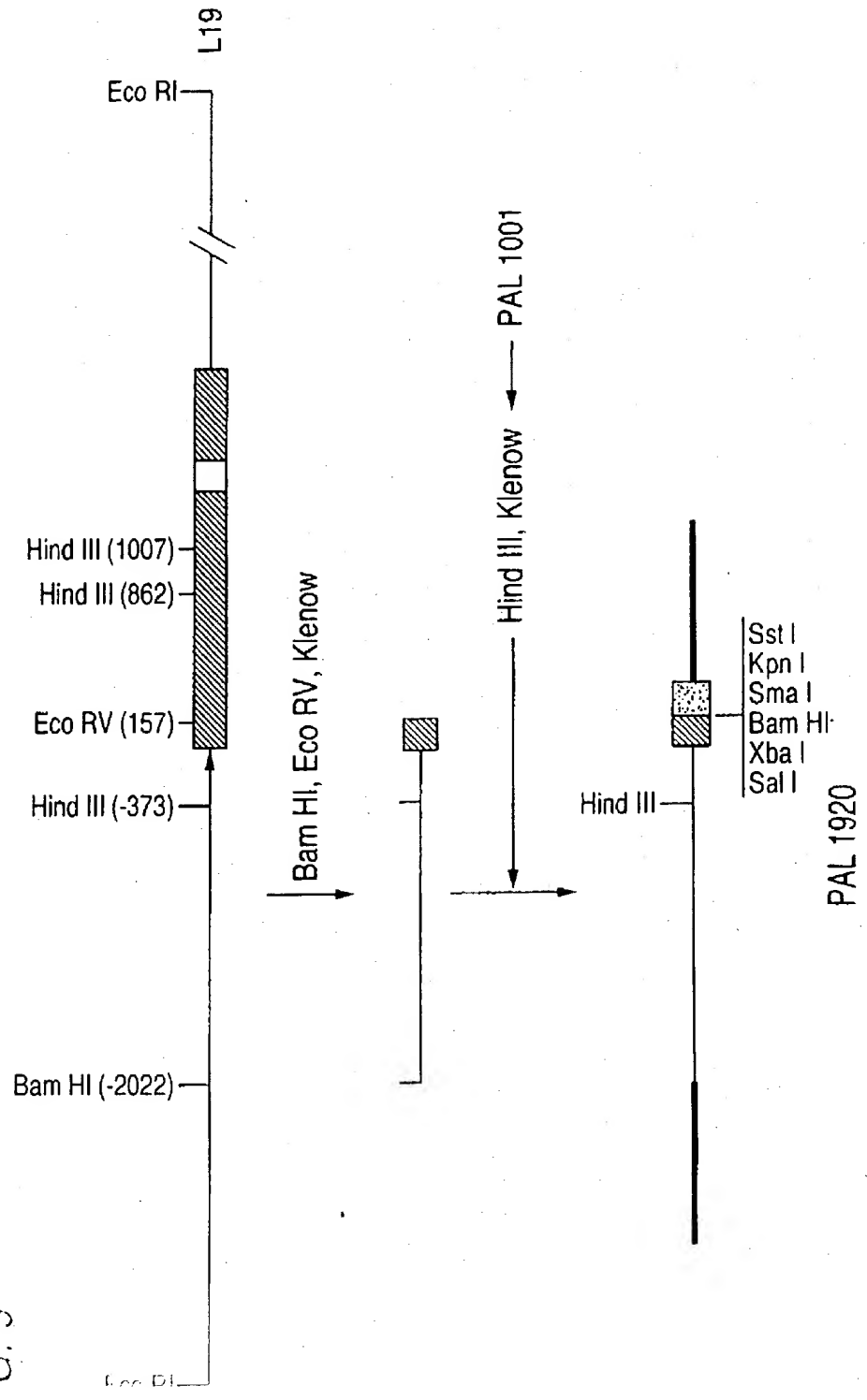

L19
Eco RI
Hind III (1007)
Hind III (862)
Eco RV (157)
Hind III (-373)
Bam HI (-2022)
Eco RI
Bam HI, Eco RV, Klenow
Hind III, Klenow
PAL 1001
Hind III
Sst I
Kpn I
Sma I
Bam HI
Xba I
Sal I
PAL 1920

FIG. 9

FIG. 10

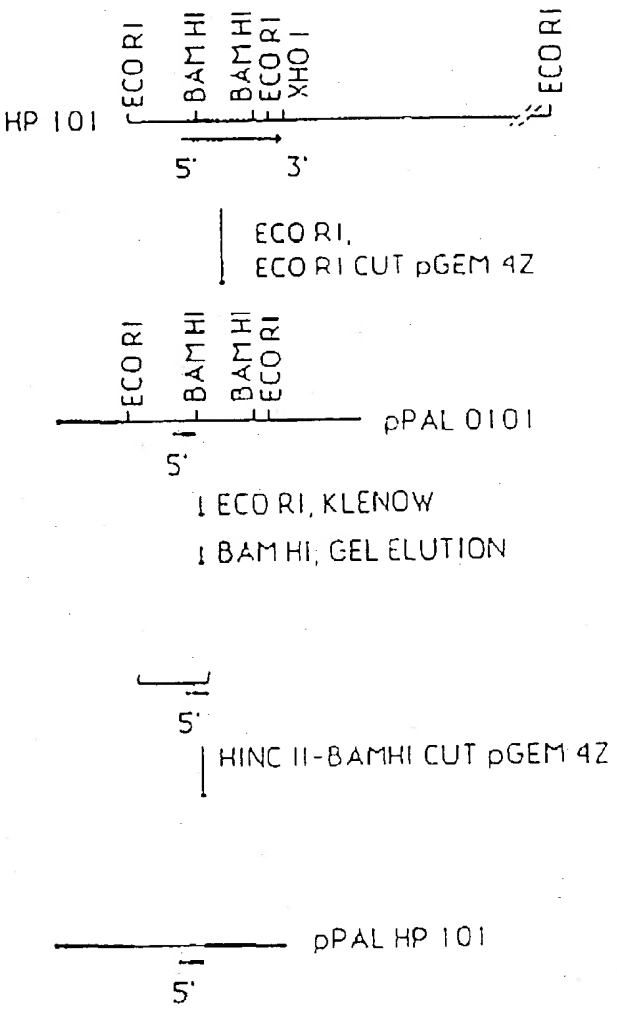

HP 101
ECO RI
BAM HI
BAM HI
ECO RI
XHO I
ECO RI
5'
3'
ECO RI,
ECO RI CUT pGEM 4Z
ECO RI
BAM HI
BAM HI
ECO RI
pPAL 0101
5'
ECO RI, KLENOW
BAM HI, GEL ELUTION
5'
HINC II-BAMHI CUT pGEM 4Z
pPAL HP 101
5'

FIG. 11

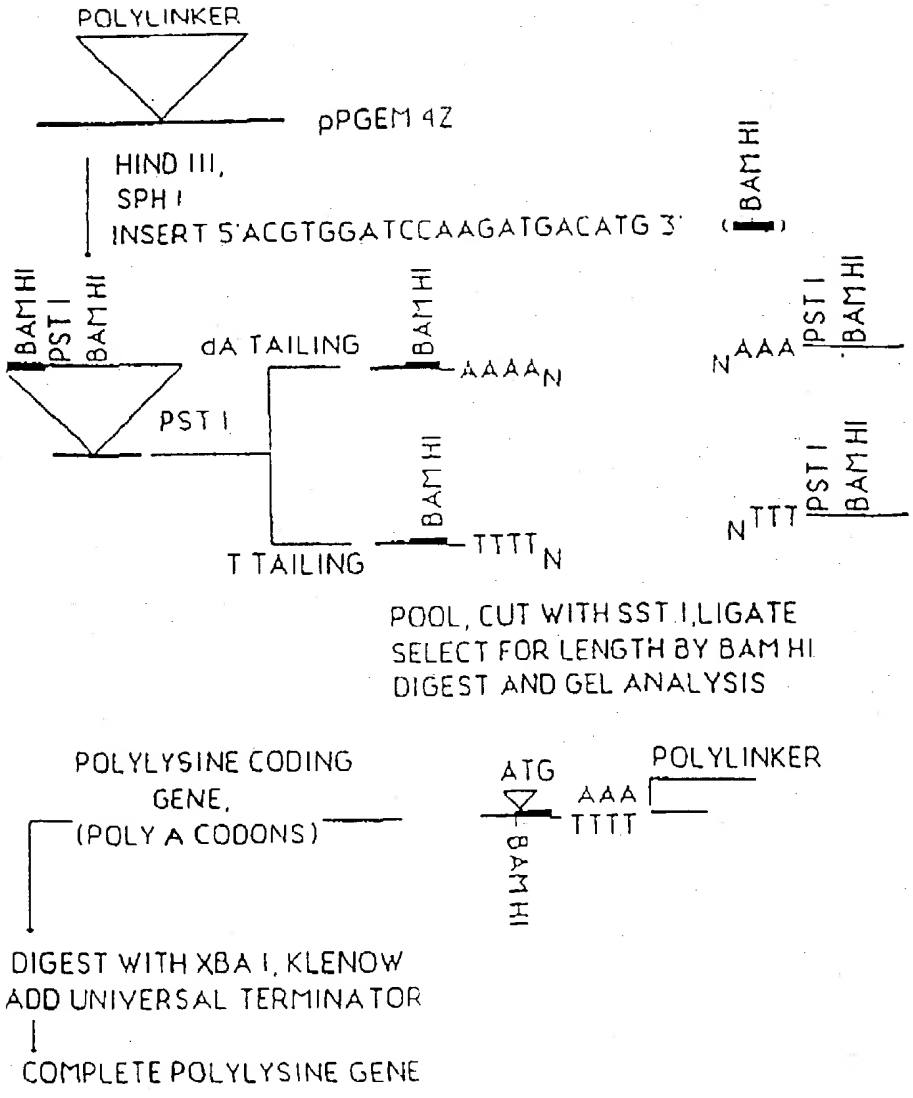

POLYLINKER
pPGEM 4Z
HIND III,
SPH I
INSERT 5'ACGTGGATCCAAGATGACATG 3'
BAM HI
PST I
BAM HI
dA TAILING
BAM HI
AAAA N
PST I
BAM HI
T TAILING
TTTT N
N AAA
PST I
BAM HI
N TTT
PST I
BAM HI
POOL, CUT WITH SST I, LIGATE
SELECT FOR LENGTH BY BAM HI
DIGEST AND GEL ANALYSIS
POLYLYSINE CODING
GENE,
(POLY A CODONS)
ATG
AAA
TTTT
POLYLINKER
BAM HI
DIGEST WITH XBA I, KLENOW
ADD UNIVERSAL TERMINATOR
COMPLETE POLYLYSINE GENE

FIG. 12

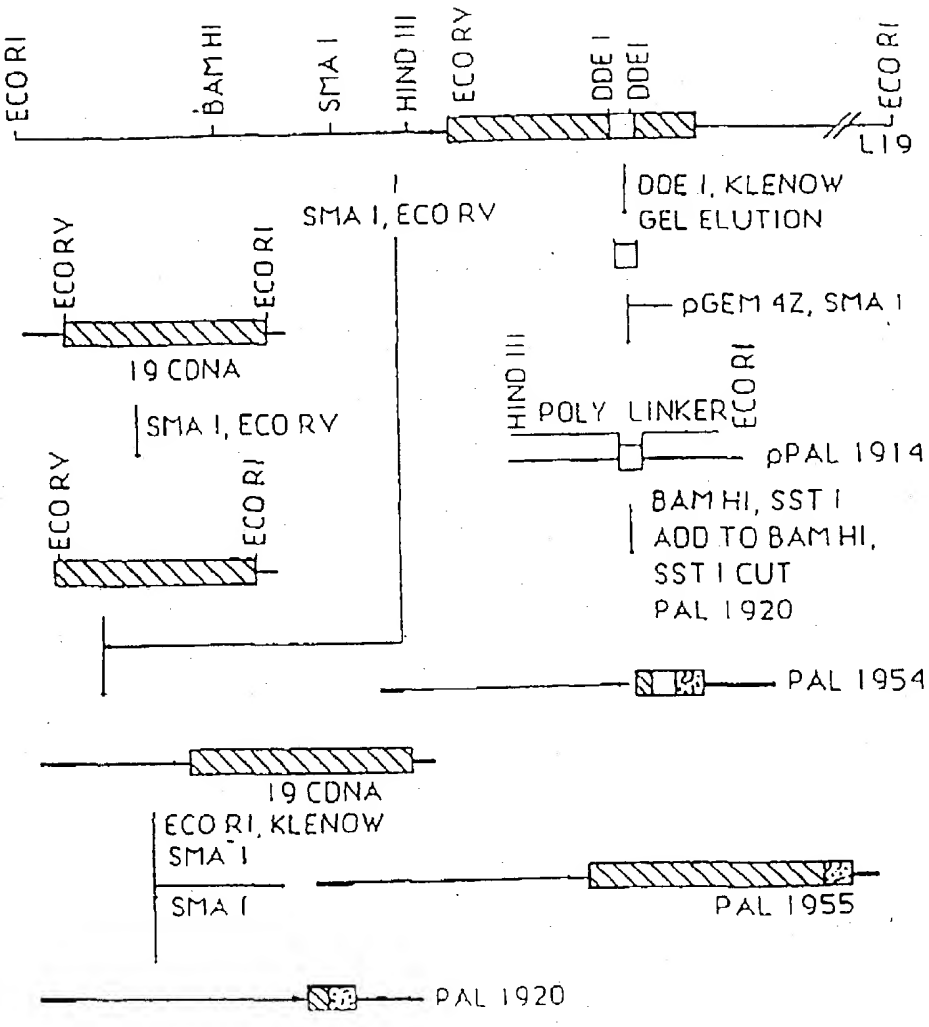

ECO RI
BAM HI
SMA I
HIND III
ECO RV
DDE I
DDE I
ECO RI
L19
SMA I, ECO RV
DDE I, KLENOW
GEL ELUTION
pGEM 4Z, SMA I
ECO RV
ECO RI
19 CDNA
SMA I, ECO RV
HIND III
POLY LINKER
ECO RI
pPAL 1914
ECO RV
ECO RI
BAM HI, SST I
ADD TO BAM HI,
SST I CUT
PAL 1920
PAL 1954
19 CDNA
ECO RI, KLENOW
SMA I
SMA I
PAL 1955
PAL 1920

FIG. 13

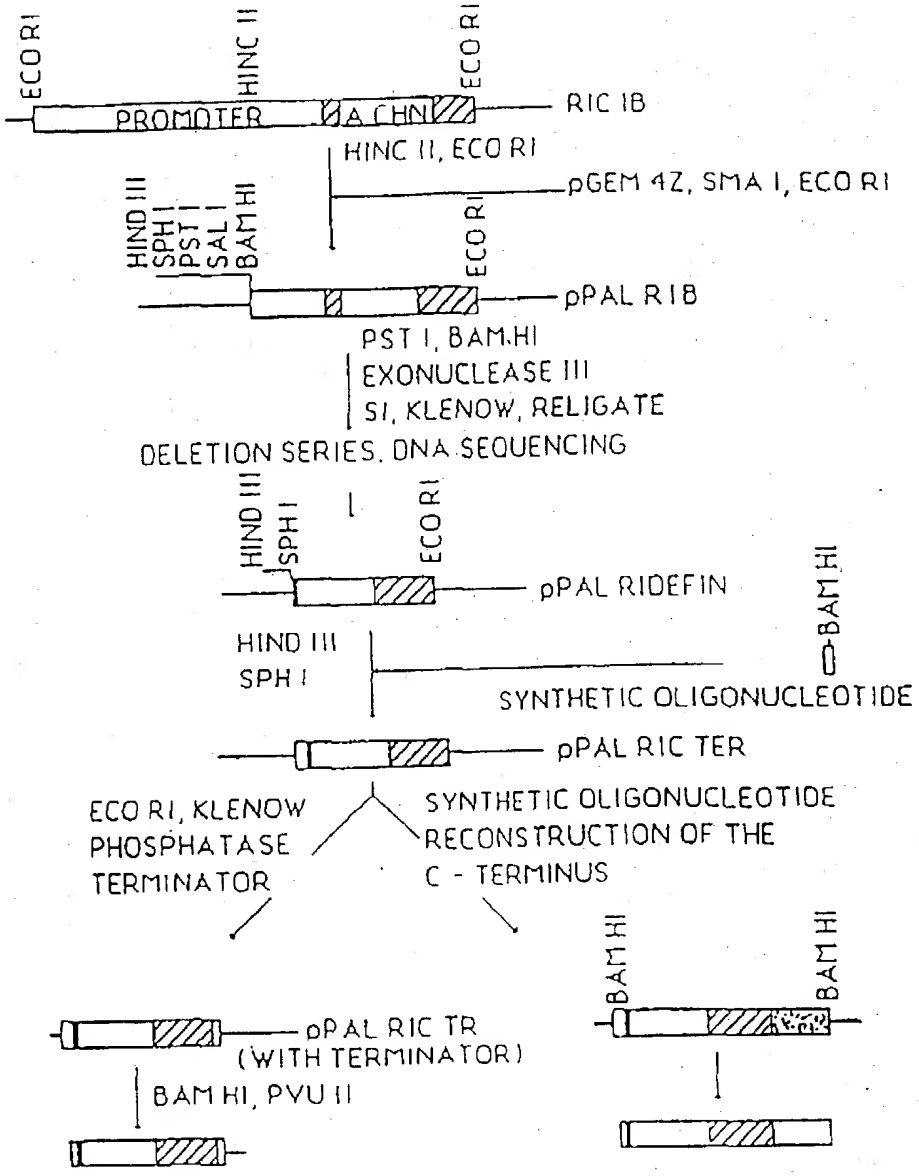

ECO RI
HINC II
ECO RI
PROMOTER
A CHN
RIC 1B
HINC II, ECO RI
pGEM 4Z, SMA I, ECO RI
HIND III
SPH I
PST I
SAL I
BAM HI
ECO RI
pPAL R1B
PST I, BAM.HI
EXONUCLEASE III
S1, KLENOW, RELIGATE
DELETION SERIES. DNA SEQUENCING
HIND III
SPH I
ECO RI
pPAL RIDEFIN
BAM HI
HIND III
SPH I
SYNTHETIC OLIGONUCLEOTIDE
pPAL RIC TER
ECO RI, KLENOW
PHOSPHATASE
TERMINATOR
SYNTHETIC OLIGONUCLEOTIDE
RECONSTRUCTION OF THE
C - TERMINUS
BAM HI
BAM HI
pPAL RIC TR
(WITH TERMINATOR)
BAM HI, PVU II

FIG. 14

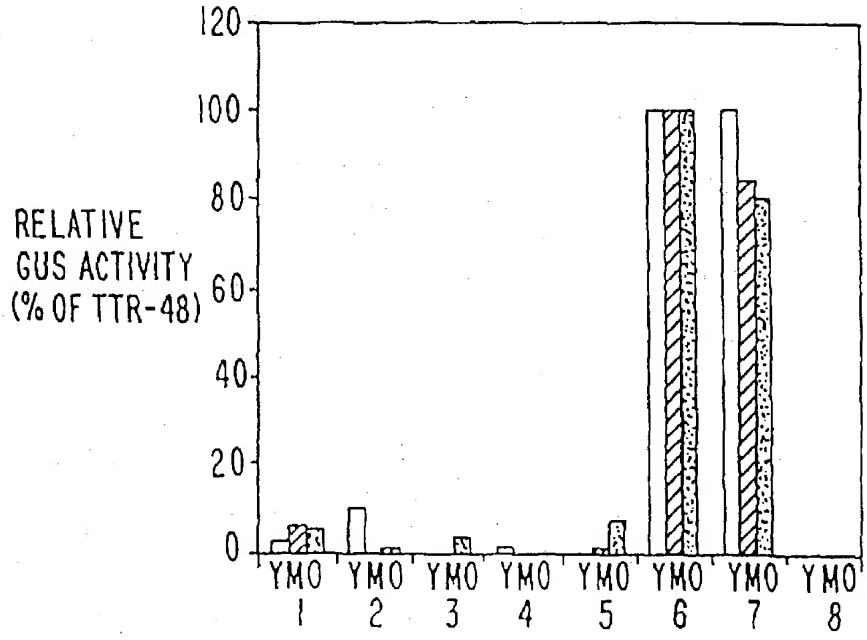

RELATIVE
GUS ACTIVITY
(% OF TTR-48)
120
100
80
60
40
20
0
YMO 1
YMO 2
YMO 3
YMO 4
YMO 5
YMO 6
YMO 7
YMO 8

FIG. 15A

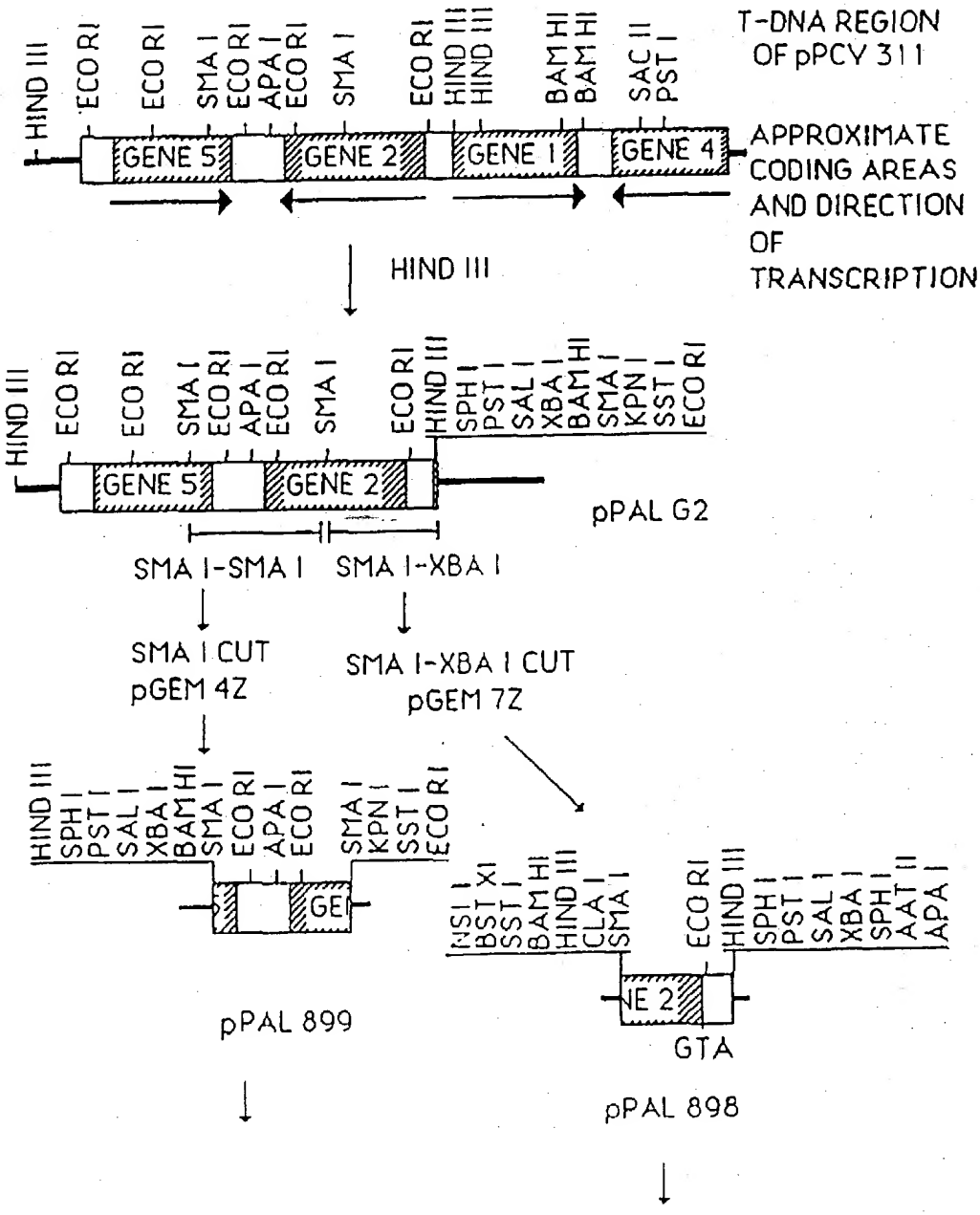

HIND III
ECO RI
ECO RI
SMA I
ECO RI
APA I
ECO RI
SMA I
ECO RI
HIND III
HIND III
BAM HI
BAM HI
SAC II
PST I
T-DNA REGION OF pPCY 311
GENE 5
GENE 2
GENE 1
GENE 4
APPROXIMATE CODING AREAS AND DIRECTION OF TRANSCRIPTION
HIND III
SPH I
PST I
SAL I
XBA I
BAM HI
SMA I
KPN I
SST I
ECO RI
pPAL G2
SMA I-SMA I
SMA I-XBA I
SMA I CUT
pGEM 4Z
SMA I-XBA I CUT
pGEM 7Z
pPAL 899
pPAL 898
GTA

FIG. 15B

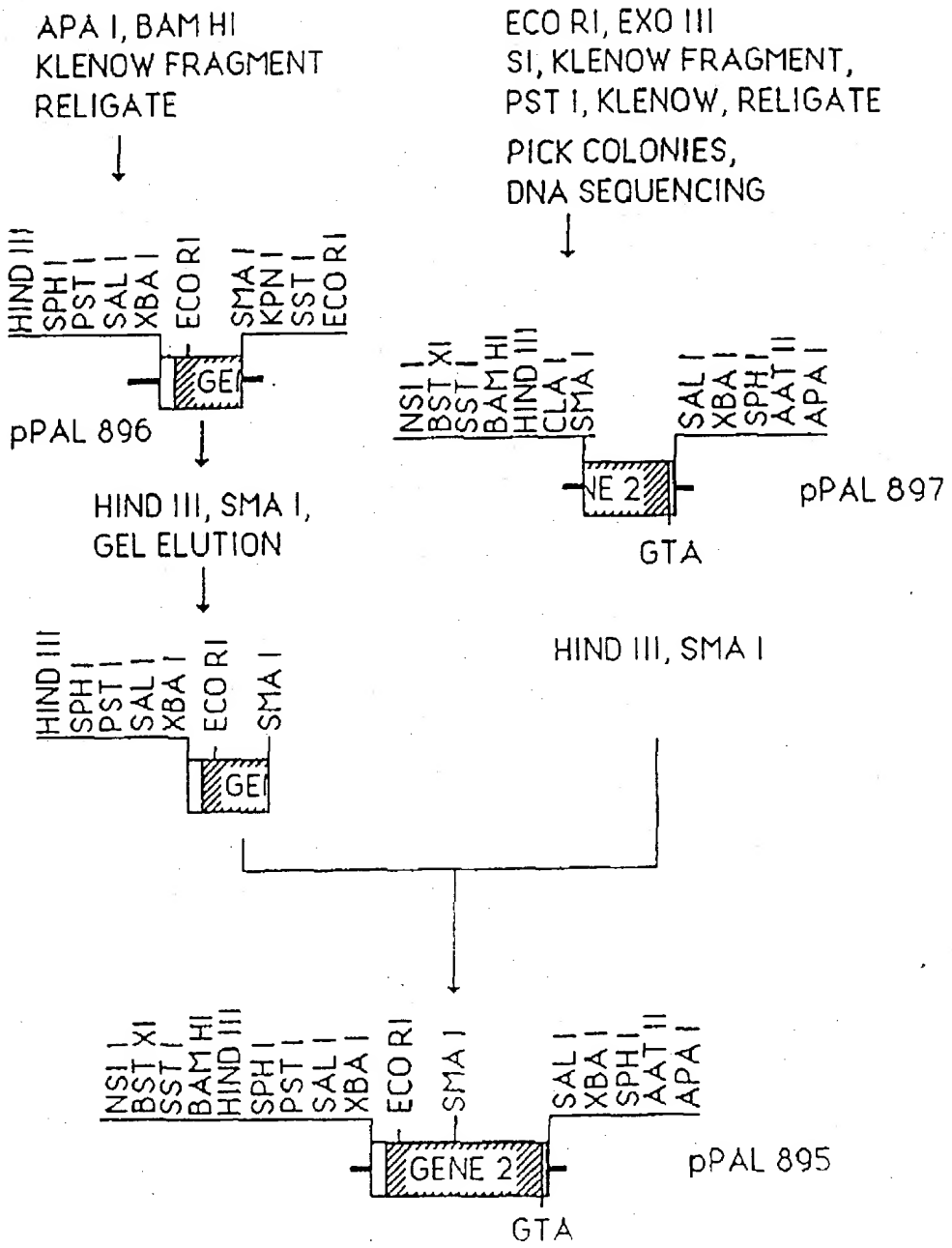

APA I, BAM HI
KLENOW FRAGMENT
RELIGATE
ECO RI, EXO III
SI, KLENOW FRAGMENT,
PST I, KLENOW, RELIGATE
PICK COLONIES,
DNA SEQUENCING
HIND III
SPH I
PST I
SAL I
XBA I
ECO RI
SMA I
KPN I
SST I
ECO RI
GE
pPAL 896
NSI I
BST XI
SST I
BAM HI
HIND III
CLA I
SMA I
SAL I
XBA I
SPH I
AAT II
APA I
NE 2
pPAL 897
GTA
HIND III, SMA I,
GEL ELUTION
HIND III
SPH I
PST I
SAL I
XBA I
ECO RI
SMA I
GE
HIND III, SMA I
NSI I
BST XI
SST I
BAM HI
HIND III
SPH I
PST I
SAL I
XBA I
ECO RI
SMA I
SAL I
XBA I
SPH I
AAT II
APA I
GENE 2
pPAL 895
GTA

FIG. 16

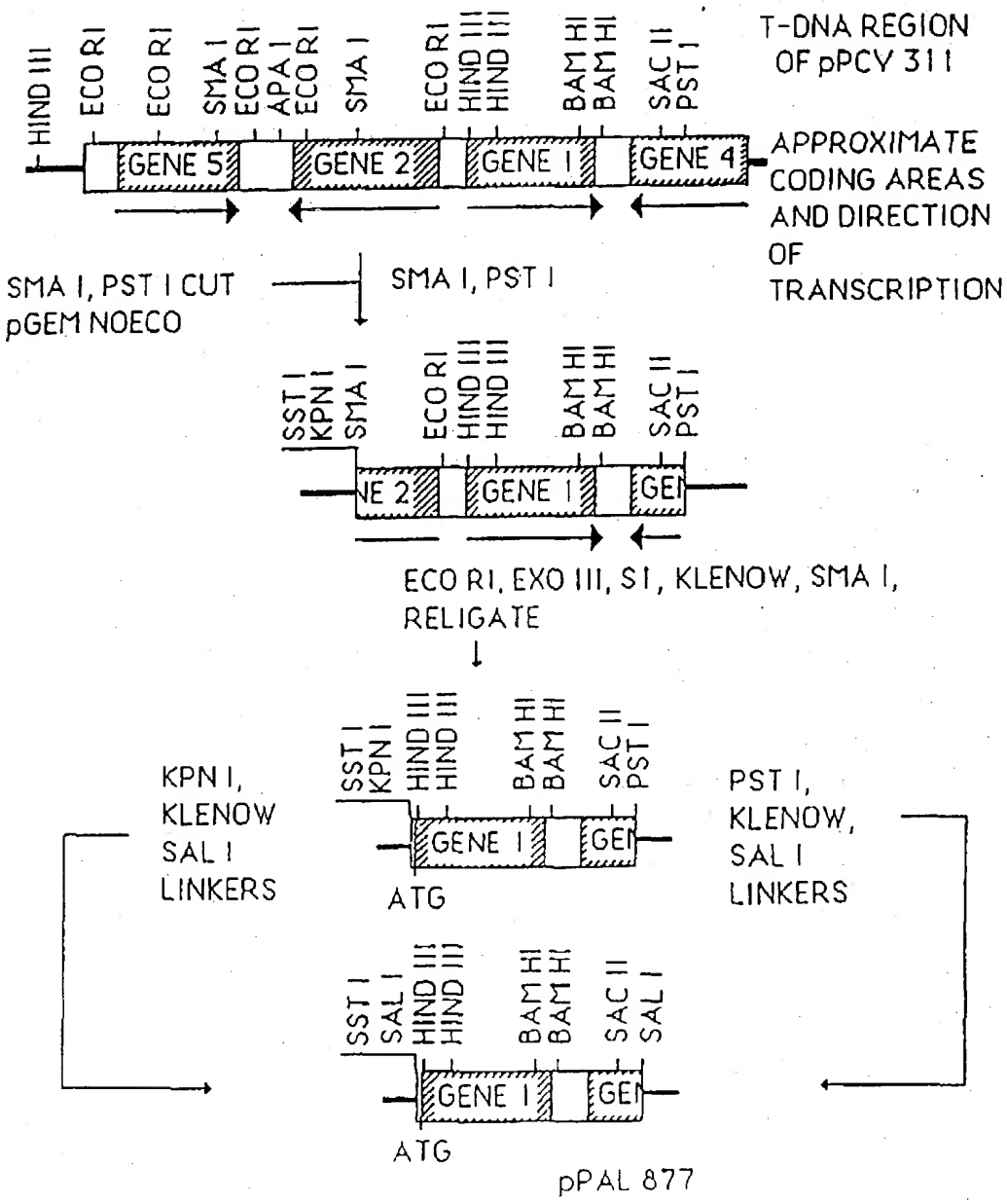

HIND III
ECO RI
ECO RI
SMA I
ECO RI
APA I
ECO RI
SMA I
ECO RI
HIND III
HIND III
BAM HI
BAM HI
SAC II
PST I
T-DNA REGION OF pPCV 311
GENE 5
GENE 2
GENE 1
GENE 4
APPROXIMATE CODING AREAS AND DIRECTION OF TRANSCRIPTION
SMA I, PST I CUT pGEM NOECO
SMA I, PST I
SST I
KPN I
SMA I
ECO RI
HIND III
HIND III
BAM HI
BAM HI
SAC II
PST I
NE 2
GENE 1
GEI
ECO RI, EXO III, S1, KLENOW, SMA I, RELIGATE
KPN I, KLENOW SAL I LINKERS
SST I
KPN I
HIND III
HIND III
BAM HI
BAM HI
SAC II
PST I
GENE 1
GEI
ATG
PST I, KLENOW, SAL I LINKERS
SST I
SAL I
HIND III
HIND III
BAM HI
BAM HI
SAC II
SAL I
GENE 1
GEI
ATG
pPAL 877

FIG. 17

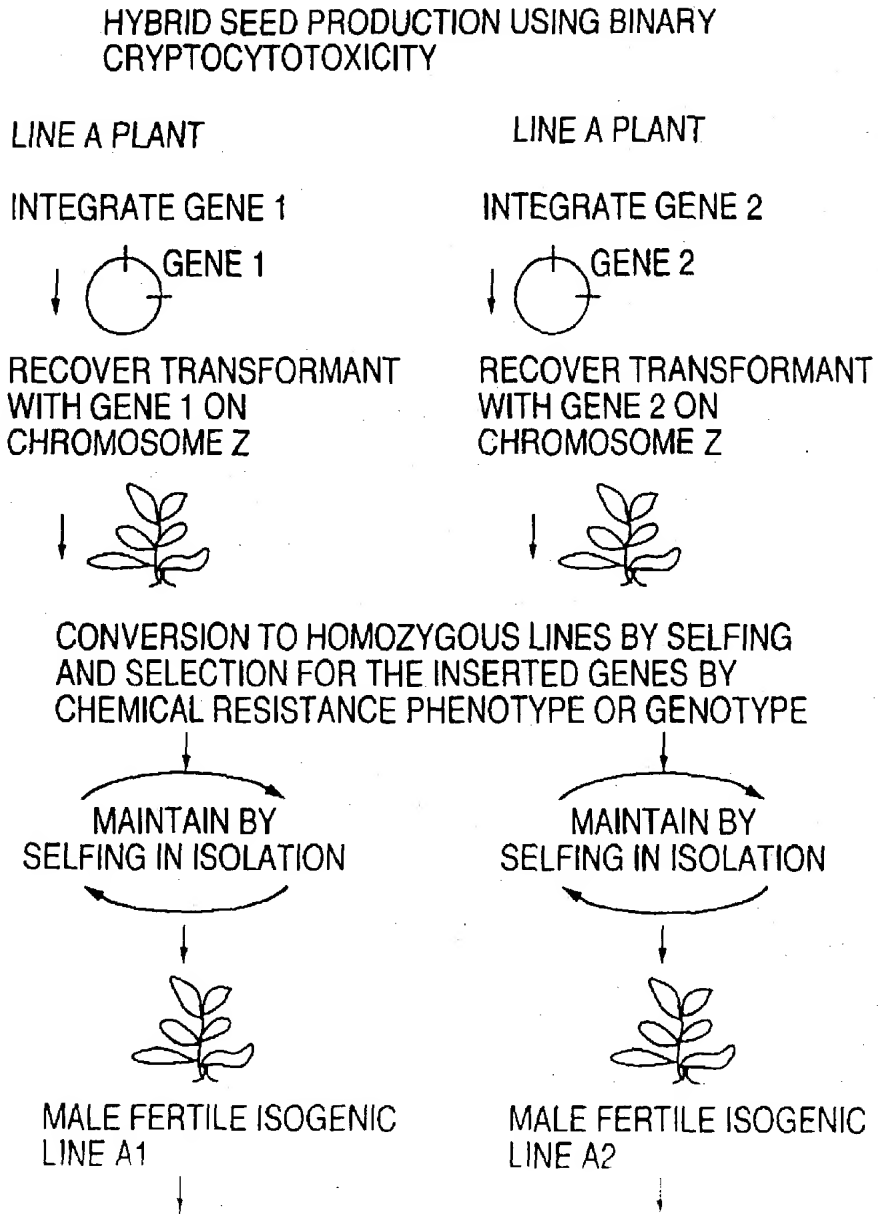

HYBRID SEED PRODUCTION USING BINARY CRYPTOCYTOTOXICITY
LINE A PLANT
INTEGRATE GENE 1
GENE 1
RECOVER TRANSFORMANT WITH GENE 1 ON CHROMOSOME Z
LINE A PLANT
INTEGRATE GENE 2
GENE 2
RECOVER TRANSFORMANT WITH GENE 2 ON CHROMOSOME Z
CONVERSION TO HOMOZYGOUS LINES BY SELFING AND SELECTION FOR THE INSERTED GENES BY CHEMICAL RESISTANCE PHENOTYPE OR GENOTYPE
MAINTAIN BY SELFING IN ISOLATION
MAINTAIN BY SELFING IN ISOLATION
MALE FERTILE ISOGENIC LINE A1
MALE FERTILE ISOGENIC LINE A2

FIG. 18

SEGREGATION OF BINARY CRYPTOCYTOTOXICITY GENES IF BOTH GENES ARE LOCATED ON THE SAME CHROMOSOME OF A CHROMOSOME PAIR IN THE ISOGENIC MALE STERILE LINE

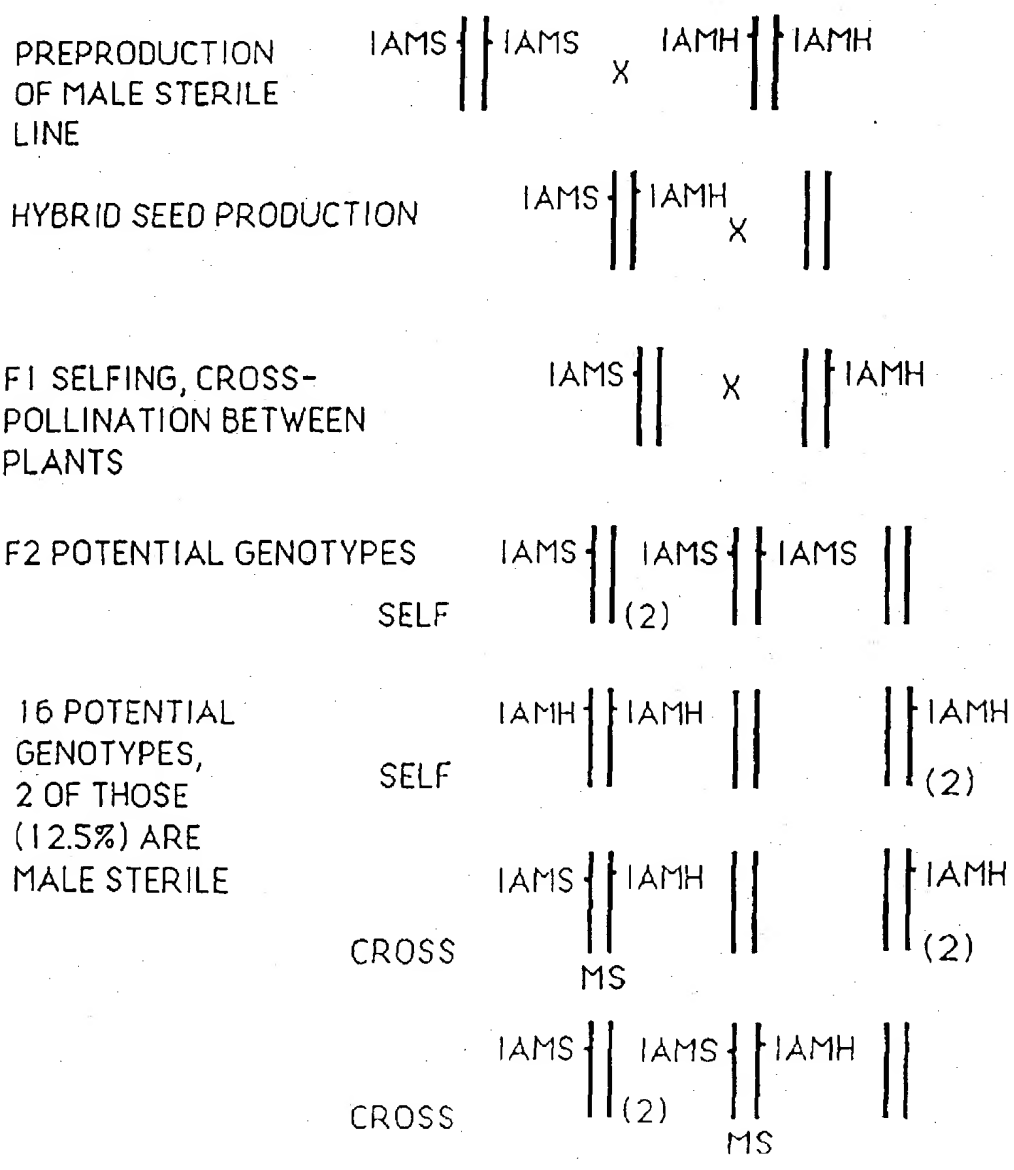
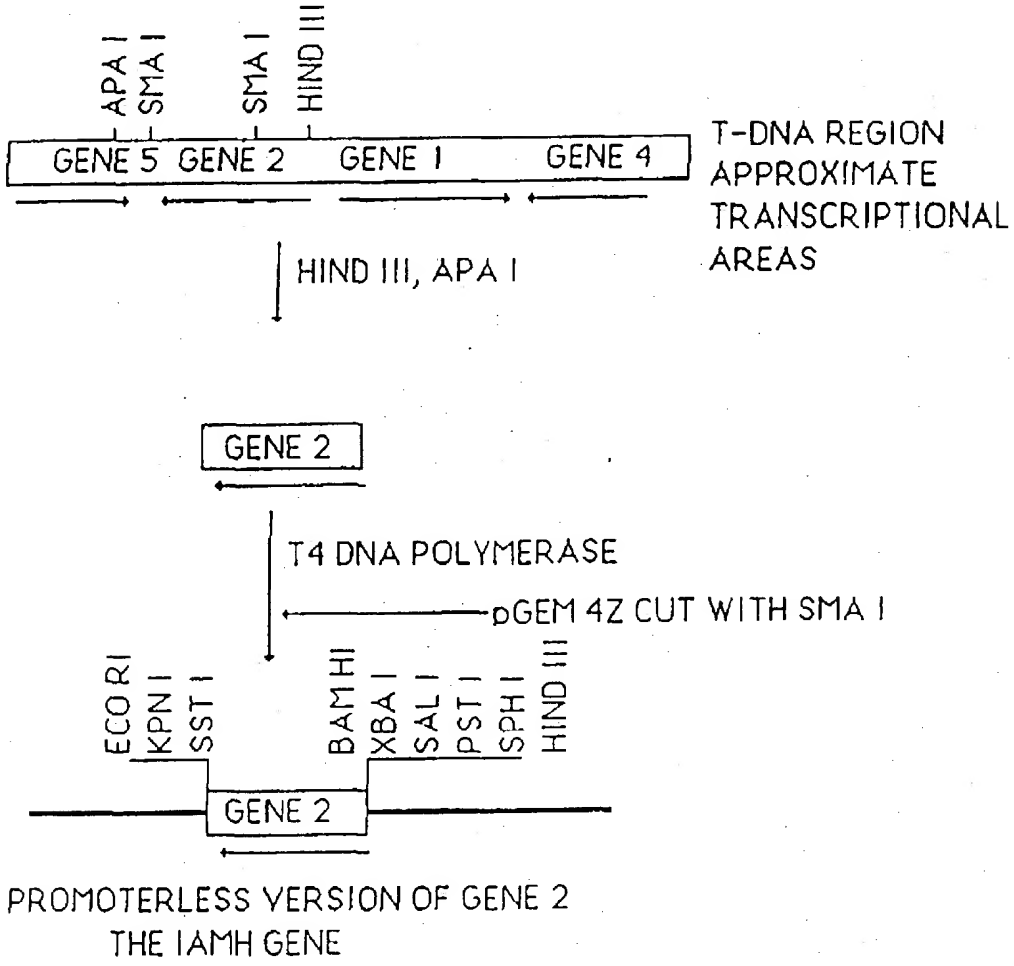


FIG. 19



PROMOTERLESS VERSION OF GENE 2
THE IAMH GENE